

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:06:38 ; Search time 173.932 Seconds
(without alignments)
1250.845 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

aa 679-714
aa 700-714

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	4058	100.0	770	1	AAP94775	Aap94775 Novel amy
2	4058	100.0	770	2	AAR41546	Aar41546 Mutated A
3	4058	100.0	770	2	AAR63442	Aar63442 Amyloid p
4	4058	100.0	770	2	AAW40130	Aaw40130 Human APP
5	4058	100.0	770	2	AAW97996	Aaw97996 Human amy
6	4058	100.0	770	4	AAE11762	Aae11762 Human amy
7	4058	100.0	770	4	AAE10648	Aae10648 Human amy
8	4058	100.0	770	4	AAE06893	Aae06893 Human amy
9	4058	100.0	770	4	AAE02600	Aae02600 Human amy

10	4058	100.0	770	4	AAU06622	Aau06622	Human par
11	4058	100.0	770	5	ABG94279	Abg94279	Amyloid b
12	4058	100.0	770	5	ABB78609	Abb78609	Human APP
13	4058	100.0	770	5	ABG76936	Abg76936	Humanised
14	4058	100.0	770	5	AAG68317	Aag68317	Human amy
15	4058	100.0	770	5	ABG80591	Abg80591	Human amy
16	4058	100.0	770	5	ABG32723	Abg32723	Human amy
17	4058	100.0	770	6	ABP72693	Abp72693	Human amy
18	4058	100.0	770	6	ABR43902	Abr43902	Beta-amy
19	4058	100.0	770	6	ABP97885	Abp97885	Amino aci
20	4058	100.0	770	6	ABR61931	Abr61931	Human amy
21	4058	100.0	772	4	AAU07223	Aau07223	Human bet
22	4058	100.0	772	4	AAE10650	Aae10650	Human amy
23	4058	100.0	772	4	AAE06895	Aae06895	Human amy
24	4058	100.0	772	4	AAE02602	Aae02602	Human amy
25	4058	100.0	772	4	AAU06624	Aau06624	Human Amy
26	4058	100.0	772	5	ABB78611	Abb78611	Human APP
27	4054	99.9	770	2	AAR62505	Aar62505	Amyloid p
28	4053	99.9	770	2	AAW19485	Aaw19485	APP770 mu
29	4053	99.9	770	2	AAW19482	Aaw19482	APP770 mu
30	4053	99.9	770	2	AAW19497	Aaw19497	APP770 mu
31	4053	99.9	770	2	AAW19500	Aaw19500	APP770 mu
32	4053	99.9	770	4	AAE06913	Aae06913	Human amy
33	4053	99.9	770	5	ABB78008	Abb78008	Amino aci
34	4050	99.8	770	4	AAE06912	Aae06912	Human amy
35	4047	99.7	768	5	AAU80959	Aau80959	Human amy
36	4047	99.7	770	2	AAW19491	Aaw19491	APP770 mu
37	4047	99.7	770	2	AAW19506	Aaw19506	APP770 mu
38	4046	99.7	770	2	AAR26340	Aar26340	APP770. 3
39	4046	99.7	770	2	AAW19488	Aaw19488	APP770 mu
40	4046	99.7	770	2	AAW19503	Aaw19503	APP770 mu
41	4039	99.5	770	2	AAR05717	Aar05717	NAP gene
42	3943.5	97.2	751	2	AAR10022	Aar10022	Beta-amy
43	3943.5	97.2	751	2	AAR20328	Aar20328	Sequence
44	3943.5	97.2	751	2	AAy08615	Aay08615	Human bet
45	3943.5	97.2	751	2	AAy08605	Aay08605	Human bet

ALIGNMENTS

RESULT 1

AAP94775

ID AAP94775 standard; protein; 770 AA.

XX

AC AAP94775;

XX

DT 25-MAR-2003 (revised)

DT 05-JUL-1990 (first entry)

XX

DE Novel amyloid precursor protein (NAP).

XX

KW SPAP; amyloid precursor protein; dysbolism; INS76; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Active-site 289. .345
 FT /*tag= -a
 FT /label= INS76
 XX
 PN EP304013-A.
 XX
 PD 22-FEB-1989.
 XX
 PF 16-AUG-1988; 88EP-00113283.
 XX
 PR 15-AUG-1987; 87JP-00203298.
 PR 21-AUG-1987; 87JP-00207995.
 PR 18-NOV-1987; 87JP-00291404.
 PR 11-DEC-1987; 87JP-00313228.
 PR 05-FEB-1988; 88JP-00025260.
 PR 10-FEB-1988; 88JP-00029366.
 PR 19-FEB-1988; 88JP-00037905.
 PR 25-MAY-1988; 88JP-00125660.
 XX
 PA (ASAH) ASAHI KASEI KOGYO KK.
 XX
 PI Kitaguchi N, Takahashi Y, Tokushima Y, Itoh H;
 XX
 DR WPI; 1989-055458/08.
 DR N-PSDB; AAN91049.
 XX
 PT Human senile plaque amyloid precursor protein and DNA - used for study
 PT and diagnosis of dysbolism in the central nervous system.
 XX
 PS Disclosure; Page; 108pp; English.
 XX
 CC AA. sequence from 289 to 345 encodes INS76 which is claimed as a senile
 CC plaque amyloid precursor (SPAP), useful for diagnosis of dysbolism in the
 CC CNS such as senile dementia. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 2

AAR41546

ID AAR41546 standard; protein; 770 AA.

XX

AC AAR41546;

XX

DT 25-MAR-2003 (revised)

DT 15-MAR-1994 (first entry)

XX

DE Mutated APP770 exon 17 protein fragment.

XX

KW Probe; mutation; exon 17; amyloid precursor protein; APP770;
 KW substitution; progressive presenile dementia; Alzheimer's disease;
 KW cerebral haemorrhage; cerebral amyloid angiopathy; 4 kD fragment;
 KW blood vessels; brain parenchyma; assay; processing; plaque.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers


```

FT      Misc-difference 692
FT      /note= "Position of mutation which causes abnormal
FT      processing of APP770"
XX
PN      EP561087-A1.
XX
PD      22-SEP-1993.
XX
PF      20-MAR-1992;      92EP-00400771.
XX
PR      20-MAR-1992;      92EP-00400771.
XX
PA      (INNO-) INNOGENETICS NV SA.
XX
PI      Van Broeckhoven C,  Martin J,  Hendriks L,  Cras P;
XX
DR      WPI; 1993-296442/38.
DR      N-PSDB; AAQ48860.
XX
PT      New mutant form of beta-amyloid polypeptide - related to development of
PT      cerebral haemorrhage and Alzheimer's disease, also corresp. nucleic acid,
PT      vectors, host cells and antibodies.
XX
PS      Disclosure; Fig 4; 2lpp; English.
XX
CC      This sequence is encoded by exon 17 of the amyloid precursor protein
CC      APP770. A mutation at position 2075 of the DNA sequence, a C>G
CC      substitution, causes the substitution of Ala for Gly at codon 692. This
CC      mutation has been detected in related patients with progressive presenile
CC      dementia (Alzheimer's disease) or cerebral haemorrhage due to cerebral
CC      amyloid angiopathy. It may be responsible for the deposition of a 4 kD
CC      proteolytic fragment of APP in blood vessel walls and brain parenchyma.
CC      Probes specific for the mutation (see also AAQ48858-59) can be used to
CC      assay mRNA encoding substances which cause abnormal processing of APP
CC      related to plaque formation, and to detect this specific mutation.
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 770 AA;

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Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

AAR63442

ID AAR63442 standard; protein; 770 AA.

XX

AC AAR63442;

XX

DT 25-MAR-2003 (revised)

DT 30-JUN-1995 (first entry)

XX

DE Amyloid protein precursor APP.

XX

KW Amyloid protein precursor; APP; beta-amyloid protein; gelatinase A;
 KW progelatinase A; decomposing agent; prophylaxis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 672. .711

FT /note= "beta-AP 1-40 gelatinase A cleavage sites"
 FT Cleavage-site 687. .689
 FT /label= gelatinase A
 FT Cleavage-site 701. .702
 FT /label= gelatinase A
 FT Cleavage-site 705. .706
 FT /label= gelatinase A
 XX
 PN EP622079-A2.
 XX
 PD 02-NOV-1994.
 XX
 PF 25-APR-1994; 94EP-00302924.
 XX
 PR 27-APR-1993; 93JP-00122207.
 PR 25-FEB-1994; 94JP-00051133.
 XX
 PA (ORIY) ORIENTAL YEAST CO LTD.
 XX
 PI Miyazaki K;
 XX
 DR WPI; 1994-334379/42.
 XX
 PT Gelatinase A-contg. amyloid beta protein decomposing agent - useful for
 PT prophylaxis or treatment of Alzheimer's disease.
 XX
 PS Disclosure; Fig 1; 12pp; English.
 XX
 CC AAR63442 describes the amino acid sequence of the amyloid protein
 CC precursor (APP), from which beta amyloid protein is derived (APB). An APB
 CC decomposing agent having either gelatinase A, a limited decomposate of
 CC gelatinase A, or progelatinase A as an active ingredient was developed.
 CC This agent can be used in medicine for prophylaxis and for the treatment
 CC of Alzheimer's disease. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDEDGDEVEEEAEAPYEEATERTTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEAPYEEATERTTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQM	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQM	770

RESULT 4

AAW40130

ID AAW40130 standard; protein; 770 AA.

XX

AC AAW40130;

XX

DT 03-JUN-1998 (first entry)

XX

DE Human APP770 protein.

XX

KW Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiopathy; brain;

KW membrane-spanning glycoprotein; beta-amyloid precursor protein; APP770;

KW chromosome 21; human; Alzheimers disease; AD; amyloid filament;

KW treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.

XX

OS Homo sapiens.

XX

PN WO9748983-A1.

XX

PD 24-DEC-1997.

XX
 PF 18-JUN-1997; 97WO-US010601.
 XX
 PR 18-JUN-1996; 96US-00665649.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Citron M, Selkoe DJ, Seubert PA, Schenk D;
 XX
 DR WPI; 1998-063287/06.
 DR N-PSDB; AAV10322.
 XX
 PT Identifying compounds that alter cellular production of amyloid-beta 42
 PT fragment - in vitro or in transgenic animal models, potentially useful
 PT for treatment of Alzheimer's and other amyloid deposition diseases.
 XX
 PS Disclosure; Fig 10; 86pp; English.
 XX
 CC This sequence represents the human beta-amyloid precursor protein APP770,
 CC which is a membrane-spanning glycoprotein encoded by a gene on the long
 CC arm of chromosome 21. A fragment of the APP protein is known as the
 CC amyloid-beta peptide (A-beta), also known as the beta-AP peptide, which
 CC forms the subunit of the amyloid filaments comprising senile (amyloid)
 CC plaques and the amyloid deposits in small cerebral and meningeal blood
 CC vessels (amyloid angiopathy). The A-beta peptide can be a 39-43 amino
 CC acid fragment. This invention provides methods of screening compounds for
 CC their ability to alter the production of the A-beta peptide, which is
 CC composed of >41 amino acids, alone, or in combination with the A-beta
 CC peptide composed of 40 amino acids or less. Such agents that reduce the
 CC production of the A-beta peptide are potentially useful for treatment of
 CC Alzheimers Disease or other diseases involving amyloid deposition such as
 CC Down's syndrome, hereditary cerebral haemorrhage with amyloidosis of
 CC Dutch type and advanced aging of the brain
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240

Qy	241	EADDDDEDEDGDEVEEEAEAPYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEAPYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDIQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDIQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770

RESULT 5

AAW97996

ID AAW97996 standard; protein; 770 AA.

XX

AC AAW97996;

XX

DT 21-JUN-1999 (first entry)

XX

DE Human amyloid precursor protein.

XX

KW Amyloid precursor protein; APP; human; gene targetting;

KW homologous recombination; transgenic mouse; transgenic animal;

KW animal model; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 672. .711

FT /note= "beta-amyloid domain"

XX

PN WO9909150-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 18-AUG-1997; 97WO-US014507.
 XX
 PR 18-AUG-1997; 97WO-US014507.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Wirak DO;
 XX
 DR WPI; 1999-181029/15.
 XX
 PT Modification of target nucleic acids - by homologous recombination, used
 PT particularly for introducing a humanised amyloid precursor protein gene
 PT into rodents for producing models of Alzheimer's disease.
 XX
 PS Disclosure; Page 85-88; 209pp; English.
 XX
 CC This polypeptide comprises human amyloid precursor protein (hAPP). The
 CC invention provides a novel gene targetting strategy that facilitates the
 CC introduction of one or more specific mutations into any gene in a single
 CC double reciprocal homologous recombination step. The method has been used
 CC particularly for introducing a humanised APP gene into rodents for
 CC producing animal models of Alzheimer's disease (AD). 4 Independent lines
 CC of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403) have been
 CC created using the novel gene targetting technique applied to embryonic
 CC stem cells. In each line, the mouse APP gene was modified to encode a
 CC mouse/human hybrid (m/hAPP) where amino acid residues 666-770 of APP770
 CC are encoded by human cDNA sequences instead of mouse genomic exons (exons
 CC 16-18). Within these residues, only 3 amino acid differences exist
 CC between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr
 CC and Arg-684 to His. This exon-cDNA fusion gene therefore encodes an APP
 CC containing a humanised beta-amyloid domain. Swedish, London,
 CC Swedish/London and stop mutations have also been introduced. Targetting
 CC vector sequences are provided (see AAX24730-33)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Db	181		GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241		EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241		EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361		PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361		PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421		KNLPKADKKAVIQHFQEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421		KNLPKADKKAVIQHFQEKVESLEQEAAANERQQVLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481		QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481		QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541		MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541		MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 6

AAE11762

ID AAE11762 standard; protein; 770 AA.

XX

AC AAE11762;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human amyloid precursor protein (APP).

XX

KW Human; neuroprotective; nootropic; immunostimulant; Alzheimer's disease;
 KW anticonvulsant; vaccine; gene therapy; Pick's disease; antidiabetic;
 KW systemic amyloidosis; maturity onset diabetes; Parkinson's disease;
 KW Huntington's disease; fronto-temporal dementia; encephalopathy; ALS;
 KW amyotrophic lateral sclerosis; amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1. .18
 FT /label= Signal_peptide
 FT Domain 18. .700
 FT /label= Extracellular_domain
 FT Protein 19. .770
 FT /label= Mature_human_AAP_protein
 FT Region 672. .714
 FT /note= "Abeta-42/43 core peptide"
 FT Domain 700. .723
 FT /label= Transmembrane_domain
 FT Region 714. .770
 FT /note= "C-100 fragment"
 FT Domain 723. .770
 FT /label= Intracellular_domain
 XX
 PN WO200162284-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 19-FEB-2001; 2001WO-DK000113.
 XX
 PR 21-FEB-2000; 2000DK-00000265.
 PR 01-MAR-2000; 2000US-0186295P.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Birk P, Jensen MR, Nielsen KG;
 XX
 DR WPI; 2001-589796/66.
 DR N-PSDB; AAD18754.
 XX
 PT In vivo down-regulation of amyloid protein for the treatment of
 PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
 PT subsequence and/or at least one analogue of the amyloidogenic polypeptide
 PT to the immune system.
 XX
 PS Claim 23; Page 113-116; 120pp; English.
 XX
 CC The invention relates to a method for in vivo down-regulation of amyloid
 CC protein such as beta amyloid (Abeta) in an animal, including human. The
 CC method comprising presenting to the animal's immune system an
 CC immunogenically effective amount of at least one amyloidogenic protein or
 CC its subsequence and/or at least one analogue of the amyloidogenic
 CC polypeptide. The amyloidogenic protein or its subsequence, and its
 CC analogue is useful for the preparation of an immunogenic composition
 CC comprising an adjuvant for down-regulating amyloid in an animal. They are
 CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
 CC disease or other diseases characterised by amyloid deposits. They are
 CC also useful in the treatment of systemic amyloidosis, maturity onset
 CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
 CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and prion-
 CC related transmissible spongiform encephalopathies. They are also useful
 CC for inducing production of antibodies against an amyloidogenic
 CC polypeptide. The present sequence is human amyloid precursor protein
 CC (APP)

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC 300
      |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC 300

Qy    301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      |||
Db    301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
      |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRLALENYITAL 480
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      |||
Db    481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
      |||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDDLANMISEPRISYGNDALMPSLTET 600

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      |||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      |||
Db    661 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy    721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
      |||
```

Db

721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 7

AAE10648

ID AAE10648 standard; protein; 770 AA.

XX

AC AAE10648;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human amyloid protein precursor 770 (APP770) isoform.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein 770; APP770;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

DR N-PSDB; AAD17897.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid precursor protein processing activity and alpha-secretase activity, for identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 8; Page 142-144; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Aspl alpha-secretase activity, which in turn is useful for identifying modulators of hu-Aspl alpha-secretase activity, where modulators that increase hu-Aspl alpha-secretase activity are useful for treating Alzheimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein with the substrate under acidic conditions and determining the level of hu-Aspl proteolytic activity. The present sequence is amyloid protein

CC precursor 770 (APP770) isoform from human
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHNMNVQNGKWDSDPSGTK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHNMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTTEEYCMAVCGSAMSQSLLKTTQEPLARD 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET 600

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVVHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 IKTEEISEVKMDAEFRHDSGYEVVHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy    721 VMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```

|||||
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 8

AAE06893

ID AAE06893 standard; protein; 770 AA.

XX

AC AAE06893;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein 770 (APP770) isoform.

XX

KW Human; aspartyl protease; beta-amyloid precursor protein 770; APP770;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy; chromosome 21.

XX

OS Homo sapiens.

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

DR N-PSDB; AAD13278.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PT activity.

XX

PS Claim 8; Page 171-173; 185pp; English.

XX

CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.

CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing

CC therapeutics for the treatment and prevention of Alzheimer's disease,

CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis

CC and neuronal loss. APP isoforms are also used in methods for identifying

CC inhibitors and modulators of human Asp2 activity. The invention relates

CC to a method for identifying agents that modulate the activity of human

CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 CC as a means to screen in cellular assays for the inhibitors of beta- and
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
 CC The present sequence is human wild-type amyloid precursor protein 770
 CC (APP770) isoform. APP770 gene is localised of chromosome 21

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHNMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHNMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660

QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA TVIVITL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA TVIVITL 720

QY 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN 770
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN 770

RESULT 9

AAE02600

ID AAE02600 standard; protein; 770 AA.

XX

AC AAE02600;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human amyloid precursor protein 770 (APP 770) protein.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "Encoded by GGC"

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

DR N-PSDB; AAD06770.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 8; Page 170-172; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of

CC Alzheimer's disease. The present sequence is human APP 770 protein
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      |||
Db    301 RAMISRWYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEEAERQA 420
      |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      |||
Db    481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
      |||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      |||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      |||
Db    661 IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy    721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
```


|||||
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 10

AAU06622

ID AAU06622 standard; protein; 770 AA.

XX

AC AAU06622;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human partial Amyloid precursor protein, APP770.

XX

KW Human; Aspartyl protease; Asp2; beta-secretase; nootropic;

KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KW amyloid-beta; Abeta; APP770.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "Encoded by GCC"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

DR N-PSDB; AAS11549.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Disclosure; Page 171-173; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp proteins
CC and vectors expressing them, and a polypeptide (isoform of amyloid
CC protein precursor (APP)) comprising the amino acid sequence of an APP or

CC its fragment containing an APP cleavage site recognizable by a mammalian
 CC beta-secretase, and further comprising two lysine residues at the
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
 CC fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
 CC associated with increased levels of Abeta processing is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is human APP770
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPYELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPYELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540

Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 QY 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDAIMPSTET 600
 QY 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTN 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTN 660
 QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 QY 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQR 770
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQR 770

RESULT 11

ABG94279

ID ABG94279 standard; protein; 770 AA.

XX

AC ABG94279;

XX

DT 10-DEC-2002 (first entry)

XX

DE Amyloid beta protein.

XX

KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.

XX

OS Homo sapiens.

XX

PN WO200256905-A2.

XX

PD 25-JUL-2002.

XX

PF 21-JAN-2002; 2002WO-IB000166.

XX

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0288549P.

PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.

XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX

PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 PI Piossek C;

XX

DR WPI; 2002-627351/67.

XX

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX

PS Disclosure; Page 417-419; 441pp; English.

XX

CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abetal-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;

Best Local Similarity 100.0%; Pred. No. 6.3e-289;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNDFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNDFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420

Db	361		PVKLP	TTAA	STPD	AVDK	YLETP	GDENE	HAHFQ	KAKER	LEAKH	RERMS	QVMRE	WEEA	ERQA	420
Qy	421		KNL	PKAD	KKAVI	QHFQ	EKVES	LEQE	AANER	QQLV	ETHMA	RVEAM	LNDR	RRRL	ALENY	ITAL 480
Db	421		KNL	PKAD	KKAVI	QHFQ	EKVES	LEQE	AANER	QQLV	ETHMA	RVEAM	LNDR	RRRL	ALENY	ITAL 480
Qy	481		QAV	PPR	PRHV	FNML	KKYV	RAEQ	KDRQ	HTLKH	FEHVR	MVDP	PKKA	AQIR	SQVM	THLRVIYER 540
Db	481		QAV	PPR	PRHV	FNML	KKYV	RAEQ	KDRQ	HTLKH	FEHVR	MVDP	PKKA	AQIR	SQVM	THLRVIYER 540
Qy	541		MNQ	SLSL	LYNV	PAVA	EELIQ	DEVDE	LLQKE	QNYSD	DDL	ANMI	SEPR	ISYGN	DALMP	SLTET 600
Db	541		MNQ	SLSL	LYNV	PAVA	EELIQ	DEVDE	LLQKE	QNYSD	DDL	ANMI	SEPR	ISYGN	DALMP	SLTET 600
Qy	601		KTT	VELL	PVNG	EFSL	DDLQ	PWHS	FGAD	SVPA	NTENE	VEP	VDAR	PAAD	RGLT	TRPGSGLTN 660
Db	601		KTT	VELL	PVNG	EFSL	DDLQ	PWHS	FGAD	SVPA	NTENE	VEP	VDAR	PAAD	RGLT	TRPGSGLTN 660
Qy	661		IKT	EEIS	EVKMD	AEFR	HDSG	YEVH	HQKL	VFFA	EDVGS	NKGAI	IIGLM	VGGV	VIAT	VIVITL 720
Db	661		IKT	EEIS	EVKMD	AEFR	HDSG	YEVH	HQKL	VFFA	EDVGS	NKGAI	IIGLM	VGGV	VIAT	VIVITL 720
Qy	721		VML	KKKQ	YTSI	HHGV	VEVD	AAVT	PEER	HLSK	MQQN	GYEN	PTYK	FFEQ	MQN	770
Db	721		VML	KKKQ	YTSI	HHGV	VEVD	AAVT	PEER	HLSK	MQQN	GYEN	PTYK	FFEQ	MQN	770

RESULT 12

ABB78609

ID ABB78609 standard; protein; 770 AA.

XX

AC ABB78609;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human APP770 protein sequence SEQ ID NO:55.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "encoded by GGC"

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.

DR N-PSDB; ABL52489.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.

XX

PS Disclosure; Page 142-144; 182pp; English.

XX

CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP770, which is used
CC in the exemplification of the present invention

XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;

Best Local Similarity 100.0%; Pred. No. 6.3e-289;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLPGIALLLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
          |||
Db      1 MLPGIALLLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
          |||
Db     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
          |||
Db    121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
```

Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSLLDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLLDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 13

ABG76936

ID ABG76936 standard; protein; 770 AA.

XX

AC ABG76936;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised antibody associated protein #5.

XX

KW Humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta; antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Disclosure; Page 165-167; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a humanized antibody associated protein as described
 CC in the invention
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.3e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
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Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
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Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
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Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
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Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQM QN	770

RESULT 14

AAG68317

ID AAG68317 standard; protein; 770 AA.

XX

AC AAG68317;

XX

DT 21-FEB-2002 (first entry)

XX

DE Human amyloid precursor protein (APP770) SEQ ID NO:5.

XX

KW Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;
 KW amyloid precursor protein; APP.

XX

OS Homo sapiens.

XX

PN WO200182967-A1.

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PD 08-NOV-2001.

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1

Query Match 100.0%; Score 4058; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 15

ABG80591

ID ABG80591 standard; protein; 770 AA.

XX

AC ABG80591;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human amyloid beta protein.

XX

KW Molecular antigen array; vaccine; antigen; antimicrobial;

KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;

KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;

KW adult respiratory distress syndrome; ARDS; Crohn's disease;

KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;

KW Grave's disease; systemic lupus erythematosus; osteoporosis;

KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;

KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;

KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;

KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KW enterokinase; cysteine-containing linker.

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OS Homo sapiens.

XX

PN WO200256907-A2.

XX

PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB000168.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX
 DR WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Disclosure; Page 394-396; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The present sequence is an antigen
 CC for use in the array of the invention. The antigen is modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a

CC virus like particle or bacterial protein (the scaffold protein)
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.3e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLPLGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

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Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

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Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

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Db    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

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|||||
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Job time : 178.932 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:09:23 ; Search time 52.6496 Seconds
 (without alignments)
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Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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 Maximum Match 100%
 Listing first 45 summaries

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 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4058	100.0	770	1	US-08-133-248-8	Sequence 8, Appli	
2	4058	100.0	770	1	US-08-231-940-1	Sequence 1, Appli	
3	4058	100.0	770	2	US-08-641-774-1	Sequence 1, Appli	
4	4058	100.0	770	2	US-08-104-165-3	Sequence 3, Appli	
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6	4058	100.0	770	4	US-08-464-250-3	Sequence 3, Appli	
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8	4058	100.0	770	4	US-09-548-367D-55	Sequence 55, Appl	
9	4058	100.0	770	4	US-09-551-853D-55	Sequence 55, Appl	
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23	3943.5	97.2	751	4	US-09-551-853D-57	Sequence 57, Appl
24	3943.5	97.2	751	6	5187153-2	Patent No. 5187153
25	3943.5	97.2	751	6	5223482-2	Patent No. 5223482
26	3943.5	97.2	753	4	US-09-548-372D-61	Sequence 61, Appl
27	3943.5	97.2	753	4	US-09-548-367D-61	Sequence 61, Appl
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43	3590.5	88.5	697	4	US-09-551-853D-16	Sequence 16, Appl
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45	3585.5	88.4	695	4	US-09-548-367D-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-133-248-8

; Sequence 8, Application US/08133248

; Patent No. 5525714

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: MUTATED FORM OF THE BETA-AMYLOID PRECURSOR

; TITLE OF INVENTION: PROTEIN GENE

; NUMBER OF SEQUENCES: 8

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/133,248

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-133-248-8

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
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Db	61	TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
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Db	241	EADDDDEDDEGDVEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
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Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
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Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAERQQVLVETHMARVEAMLNDRRRRLALENYITAL	480
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QY 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 2

US-08-231-940-1

; Sequence 1, Application US/08231940
 ; Patent No. 5550216
 ; GENERAL INFORMATION:
 ; APPLICANT: MIYAZAKI, Kaoru
 ; TITLE OF INVENTION: GELATINASE A INHIBITOR
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/231,940
 ; FILING DATE: 25-APR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5-120457
 ; FILING DATE: 26-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-62129
 ; FILING DATE: 08-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NEIMARK, Sheridan
 ; REGISTRATION NUMBER: 20,520
 ; REFERENCE/DOCKET NUMBER: MIYAZAKI=4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-231-940-1

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6e-263;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60

Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

US-08-641-774-1

; Sequence 1, Application US/08641774

; Patent No. 5843695

; GENERAL INFORMATION:

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; APPLICANT: MIYAZAKI, Kaoru
; TITLE OF INVENTION: BETA-AP DECOMPOSING AGENT
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,774
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,474
; FILING DATE: 25-APR-1994
; APPLICATION NUMBER: JP 5-122207
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-51133
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEIMARK, Sheridan
; REGISTRATION NUMBER: 20,520
; REFERENCE/DOCKET NUMBER: MIYAZAKI=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-641-774-1

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Query Match          100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWSDPSGTK 60

QY     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

QY    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
 |||

Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

QY 241 EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300
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Db 241 EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAETGPC 300

QY 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
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Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

QY 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
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Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

QY 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

QY 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
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Db 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

QY 541 MNQSLSLLYNVPAAVEEQDEVDLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
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Db 541 MNQSLSLLYNVPAAVEEQDEVDLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

QY 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660

QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
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Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

QY 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN 770
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Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQRN 770

RESULT 4

US-08-104-165-3

; Sequence 3, Application US/08104165

; Patent No. 5877015

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

```

; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,165
; FILING DATE: 21-JAN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-104-165-3

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Query Match          100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

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Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

QY    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

QY    241 EADDDDEDDEDGDEVEEEAAEPPYEEATERTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC 300
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Db    241 EADDDDEDDEDGDEVEEEAAEPPYEEATERTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC 300

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Qy 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
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 Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
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 Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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 Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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 Db 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 541 MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
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 Db 541 MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
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 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
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 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
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 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 5

US-08-464-250-3

; Sequence 3, Application US/08464250

; Patent No. 6107542

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; APPLICANT: GOATE, Alison Mary

; APPLICANT: MULLAN, Michael John

; APPLICANT: CHARTIER-HARLIN, Marie-Christine

; APPLICANT: OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: .44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,250
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/104,165
; FILING DATE: 21-JAN-1992
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-250-3

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Query Match          100.0%; Score 4058; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

QY     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
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Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

QY    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
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Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

QY    241 EADDDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
        |||
Db    241 EADDDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

QY    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        |||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

QY    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
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Db 361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
 Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITAL 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRLALENYITAL 480
 Qy 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
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 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
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 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
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 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 6

US-08-464-250-3

; Sequence 3, Application US/08464250

; Patent No. 6300540

; GENERAL INFORMATION:

; APPLICANT: HARDY, John Anthony

; GOATE, Alison Mary

; MULLAN, Michael John

; CHARTIER-HARLIN, Marie-Christine

; OWEN, Michael John

; TITLE OF INVENTION: Test and Model for Alzheimer's Disease

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,250

; FILING DATE: 05-Jun-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/104,165

; FILING DATE: 21-JAN-1992

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; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-464-250-3

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Query Match          100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTTSVEEVVREVCSEQAETGPC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTTTSVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITAL 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYITAL 480

```

Qy 481 QAVPPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 QAVPPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770

RESULT 7

US-09-548-372D-55
 ; Sequence 55, Application US/09548372D
 ; Patent No. 6420534
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280I
 ; CURRENT APPLICATION NUMBER: US/09/548,372D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 55
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-548-372D-55

Query Match 100.0%; Score 4058; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6e-263;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRILNMHMNVQNGKWSDPSGTK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRILNMHMNVQNGKWSDPSGTK 60

Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 8

US-09-548-367D-55

; Sequence 55, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

```

Query Match          100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      |||
Db      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61  TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61  TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121  EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181  GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
      |||
Db    181  GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

Qy    241  EADDDDEDEDGDVEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      |||
Db    241  EADDDDEDEDGDVEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301  RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360
      |||
Db    301  RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD 360

Qy    361  PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
      |||
Db    361  PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    421  KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      |||
Db    421  KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481  QAVPPRPRHVFNMLKKYVRAEQKDROHTLKHFEHVRMVDPKKAAOIRSQVMTHLRVIYER 540

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Db      481  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 540
Qy      541  MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Db      541  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 600
Qy      601  KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db      601  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 660
Qy      661  IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Db      661  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 720
Qy      721  VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db      721  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 770

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RESULT 9

US-09-551-853D-55

; Sequence 55, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-55

Query Match 100.0%; Score 4058; DB 4; Length 770;

Best Local Similarity 100.0%; Pred. No. 6e-263;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db      1  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 60
Qy      61  TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

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Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 10

US-08-665-649-3

; Sequence 3, Application US/08665649

; Patent No. 6610493

; GENERAL INFORMATION:

; APPLICANT: CITRON, MARTIN

; APPLICANT: SELKOE, DENNIS J.

; APPLICANT: SEUBERT, PETER A.

; APPLICANT: SCHENK, DALE

```

; TITLE OF INVENTION: SCREENING COMPOUNDS FOR THE ABILITY TO
; TITLE OF INVENTION: ALTER THE PRODUCTION OF AMYLOID-BETA PEPTIDE (X-r41)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,649
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,067
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15270-000650
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-649-3

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Query Match          100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

```


Qy	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN	770

RESULT 11

US-09-548-372D-59

; Sequence 59, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL 720
Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 12

US-09-548-367D-59

; Sequence 59, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 59

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-367D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;

Best Local Similarity 100.0%; Pred. No. 6e-263;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Qy 241 EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC 300

Db	241	EADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFLDDLPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFLDDLPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN	770

RESULT 13

US-09-551-853D-59

; Sequence 59, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-59

Query Match 100.0%; Score 4058; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 6e-263;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
        |||
Db    241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        |||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
        |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
        |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEANERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
        |||
Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
        |||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600

Qy    601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
        |||
Db    601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
        |||
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Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||

Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 14

US-08-123-702-4

; Sequence 4, Application US/08123702

; Patent No. 5604131

; GENERAL INFORMATION:

; APPLICANT: Wadsworth, Samuel

; APPLICANT: Snyder, Benjamin

; APPLICANT: Reddy, Vermuri, B.

; APPLICANT: Wei, Chamer

; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770

; Patent No. 5604131

; TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; STREET: 1201 West Peachtree Street

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,702

; FILING DATE: 17-SEPT-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: TSI121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794

; TELEFAX: (404)-873-8795

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 751 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-702-4

Query Match 97.2%; Score 3943.5; DB 1; Length 751;

Best Local Similarity 97.4%; Pred. No. 2.6e-255;

Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA-----	344
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	345	---IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	402	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	461
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	600
Db	522	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET	581
Qy	601	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	KTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	642	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	701
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	702	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	751

RESULT 15

US-08-104-165-2

; Sequence 2, Application US/08104165

; Patent No. 5877015

```

; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; APPLICANT: GOATE, Alison Mary
; APPLICANT: MULLAN, Michael John
; APPLICANT: CHARTIER-HARLIN, Marie-Christine
; APPLICANT: OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,165
; FILING DATE: 21-JAN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-104-165-2

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Query Match          97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 2.6e-255;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

```


Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSA-----	344
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	345	---: IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	402	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	461
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	522	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	581
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	642	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	701
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	702	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	751

Search completed: August 13, 2004, 09:17:35
 Job time : 55.6496 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2004, 09:08:23 ; Search time 42.3077 Seconds
(without alignments)
1750.686 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query									
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3	3493.5	86.1	695	2	S00550	Alzheimer's diseas					
4	3468.5	85.5	695	2	A27485	Alzheimer's diseas					
5	3403.5	83.9	747	2	JH0773	Alzheimer's diseas					
6	2446.5	60.3	484	4	A32761	hypothetical Alzhe					
7	1981.5	48.8	763	2	A49321	amyloid beta (A4)					
8	1971.5	48.6	765	2	S42880	amyloid precursor-					
9	1956.5	48.2	751	2	A49974	beta-amyloid precu					
10	1150.5	28.4	653	2	A46362	amyloid precursor-					
11	1112.5	27.4	511	2	JC1404	CDEI-box DNA-bindi					
12	785	19.3	686	2	T15795	hypothetical prote					
13	737.5	18.2	886	2	A32758	beta-amyloid-like					

14	706	17.4	246	2	S38344	CDEI-binding prote
15	501	12.3	100	2	A32282	Alzheimer's diseas
16	411	10.1	82	2	PQ0438	Alzheimer's diseas
17	403	9.9	76	2	S06678	Alzheimer's diseas
18	397	9.8	76	2	S03607	Alzheimer's diseas
19	383	9.4	76	2	S04855	Alzheimer's diseas
20	296.5	7.3	191	2	A35981	sperm membrane pro
21	283	7.0	57	2	E60045	Alzheimer's diseas
22	283	7.0	57	2	F60045	Alzheimer's diseas
23	283	7.0	57	2	G60045	Alzheimer's diseas
24	283	7.0	57	2	D60045	Alzheimer's diseas
25	283	7.0	57	2	A60045	Alzheimer's diseas
26	283	7.0	57	2	B60045	Alzheimer's diseas
27	256.5	6.3	111	2	S41082	amyloid precursor
28	217	5.3	42	2	PN0512	beta-amyloid prote
29	194.5	4.8	2225	2	T26063	hypothetical prote
30	186	4.6	993	2	S49461	synaptonemal compl
31	183.5	4.5	396	2	S53325	tissue factor path
32	183	4.5	1188	2	T46608	zinc finger protei
33	179.5	4.4	1208	2	T27822	hypothetical prote
34	178.5	4.4	1110	2	I51116	NF-180 - sea lampr
35	177.5	4.4	2167	2	T34395	hypothetical prote
36	176.5	4.3	252	2	JG0185	hepatocyte growth
37	176	4.3	55	2	S30332	proteinase inhibit
38	175.5	4.3	579	2	JH0820	160K golgi antigen
39	175	4.3	302	1	TIRTGK	tissue factor path
40	175	4.3	1182	2	T30189	myelin transcripti
41	174.5	4.3	1271	2	A45555	glutamate rich pro
42	173.5	4.3	1087	2	T30330	gelsolin-related p
43	173.5	4.3	1558	2	C89114	protein C37C3.6a [
44	172	4.2	922	2	T23573	hypothetical prote
45	170.5	4.2	5170	2	T15348	hypothetical prote

ALIGNMENTS

RESULT 1

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775
 A;Accession: S02260
 A;Molecule type: DNA
 A;Residues: 1-288,'V',365-770 <LEM1>
 A;Cross-references: EMBL:X13466
 A;Note: alternative splice form APP(695)
 R;Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A;Reference number: S05194
 A;Accession: S05194
 A;Molecule type: DNA
 A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
 A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A;Note: alternative splice form APP(695)
 R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A;Title: Characterization of the 5'-end region and the first two exons of the
 beta-protein precursor gene.
 A;Reference number: A32277; MUID:89165870; PMID:2538123
 A;Accession: A32277
 A;Molecule type: DNA
 A;Residues: 1-75 <LAF>
 A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1;
 PID:g516074
 R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little,
 S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows
 similarity to soybean trypsin inhibitor.
 A;Reference number: A33260; MUID:89392030; PMID:2675837
 A;Accession: A33260
 A;Molecule type: DNA
 A;Residues: 656-737 <JOH>
 A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.;
 Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in
 amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein
 diagnostic assays.
 A;Reference number: A35486; MUID:90321244; PMID:2196878
 A;Accession: A35486
 A;Molecule type: DNA
 A;Residues: 672-710 <PRE1>
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A;Reference number: I39451; MUID:90236318; PMID:2110105
 A;Accession: I39452
 A;Status: nucleic acid sequence not shown; translation not shown; translated
 from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-770 <YOS1>
 A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A;Accession: I39451

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
 A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A;Reference number: A59020; MUID:91340168; PMID:1908403
 A;Contents: annotation; erratum
 A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
 A;Reference number: I39453; MUID:90260663; PMID:2111584
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
 A;Reference number: I59562; MUID:92022553; PMID:1925564
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 689-716,'F',718-737 <MUR>
 A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
 A;Reference number: A44017; MUID:93035397; PMID:1415269
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692,'G',694-718 <KAM1>
 A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A;Experimental source: familial Alzheimer disease family LIT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
 Nature 325, 733-736, 1987

A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288,'V',365-770 <KAN>
 A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
 A;Reference number: A29030; MUID:87231971; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
 A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756,'S',758-770 <GOL>
 A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYR>
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344,'I',365-366 <TAN2>
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612

A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.;
 Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase
 inhibitors.
 A;Reference number: S00925; MUID:88122639; PMID:2893289
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344,'I',365-770 <PO2>
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1;
 PID:g28721
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease
 inhibitory activity.
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer,
 B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of
 three patients with sporadic Alzheimer's disease.
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-770 <VIT1>
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288,'V',365-770 <VIT2>
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.;
 Marotta, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 disease brain: coding and noncoding regions of the fetal precursor mRNA are
 expressed in the cortex.
 A;Reference number: A31087; MUID:88124954; PMID:2893379
 A;Accession: A31087
 A;Molecule type: mRNA
 A;Residues: 507-770 <ZAI>
 A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for
 residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT

for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
 A;Note: the cited Genbank accession number, J03594, is not in release 101.0
 R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.6e-210;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHNMVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLMHNMVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTET	600
Qy	601	KTTVELLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVVEEVREVCSEQAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVVEEVR-----	288
Qy	301	RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	289	-----	288
Qy	361	PVKLPETTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	289	---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	345

QY 421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
 |||
 Db 346 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 405
 QY 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||
 Db 406 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 465
 QY 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
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 Db 466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 525
 QY 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||
 Db 526 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 585
 QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Db 586 IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
 QY 721 VMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||
 Db 646 VMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.

A;Reference number: S00550; MUID:88312583; PMID:2900758

A;Accession: S00550

A;Molecule type: mRNA

A;Residues: 1-695 <SHI>

A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617

R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.

A;Reference number: A41245; MUID:88264430; PMID:2968652

A;Accession: A41245

A;Molecule type: protein

A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A;Note: evidence for heparan sulfate attachment

R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.

A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites

A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 86.1%; Score 3493.5; DB 2; Length 695;
Best Local Similarity 87.7%; Pred. No. 8.6e-180;
Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIGTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDSIDSADAEEDDSVWVGADTDYADGGEDKVVEVAEEEEVADVEEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
		:	
Db	241	EAEDDEDVEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVR-----	288
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	289	-----	288
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
		:	
Db	289	---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	345
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	346	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	405
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	406	QAVPPRPHHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	465

QY 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTET 600
 |||
 Db 466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGN DALMPSLTET 525
 QY 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||
 Db 526 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585
 QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Db 586 IKTEEISEVKMDAEFGHDSGFVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645
 QY 721 VMLKKKQYTSIIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||
 Db 646 VMLKKKQYTSIIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 4

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999

C;Accession: A27485; S19727; I49485

R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A;Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085

A;Experimental source: brain

R;de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A;Reference number: S19727; MUID:92096458; PMID:1756177

A;Accession: S19727

A;Molecule type: mRNA

A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>

A;Cross-references: EMBL:X59379

R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.

Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A;Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329

C;Genetics:

A;Map position: 16C3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 85.5%; Score 3468.5; DB 2; Length 695;
Best Local Similarity 87.3%; Pred. No. 1.9e-178;
Matches 672; Conservative 6; Mismatches 17; Indels 75; Gaps 1;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNHMHMNVQNGKWESDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDSVDSADAEEEDSDVWWVGADTDYADGGEDKVVEVAEEEEVADVVEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 EADDDDEDVEDGDEVEEEAEPEYEEATERTTSTATTTTTTTESVEEVVR----- 288

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARD 360
Db    289 ----- 288

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
      :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 345

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLDLENYIIAL 405

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    406 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTHLRVIYER 465

Qy    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    466 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 525

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    526 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 585

Qy    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    586 IKTEEISEVKMDAEFGHDSGFVVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 645

Qy    721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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Db

JH0773

Query Match 83.9%; Score 3403.5; DB 2; Length 747;
Best Local Similarity 85.2%; Pred. No. 6.2e-175;
Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGRLLNMHMNVQNGKWDSDPSGKTCTCIDTKEGILQYCQE	75
		:	
Db	15	ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVGEFVSDALLVPDKCKF	135
		: : :	
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF	131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN	195
		: : : : :	
Db	132	LHQERMDICETHLHWHTVAKESCSEKSMLEHYGMLLPCGIDKFRGVEFVCCPSAEES	191
Qy	196	VDSADAAEEDSDVWGGADTDYADGSEDKVVEVA--EEEEVAEVEEEEADDEDDEDGDE	253
		:	
Db	192	FDSADAAEDDCDVWGGADADYVDRSDDKAVEAQPDEEEVEVEVEEETDDDED--DGDE	249
Qy	254	VEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYFDVTE	313
		:	
Db	250	AEEPEPEPYEEATERTTTSIATTTTTTTTESVEEVVREVCSEQAETGPCRAMISRWYDVTE	309
Qy	314	GKCAPFFYGGCGGNRNNFDEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPPTAASTPD	373
		: : :	
Db	310	SKCAQFIYGGCGGNRNNFESDDYCMVCGSV-----IPATAASTPD	350
Qy	374	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQ	433
		: : :	
Db	351	AVDKYLENPNDENEHDFLKAKEKLEKGRHEKRMSEVMKEWEEAERQAKNLPKADKKAVIO	410

[illegible]

Qy 200 DAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEEEEADDEDEDGDEVEEEAE 259
 |||
 Db 121 DAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEEEEADDEDEDGDEVEEEAE 180
 Qy 260 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPCRAMISRWFYFDVTEGKCAPF 319
 |||
 Db 181 EPYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPCRAMISRWFYFDVTEGKCAPF 240
 Qy 320 FYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPTTAASTPDAVDKYL 379
 ||| :|||
 Db 241 FYGGCGGNRNNFDTEEYCMVCGSA-----IPTTAASTPDAVDKYL 281
 Qy 380 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 439
 |||
 Db 282 ETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKV 341
 Qy 440 ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLKKYVR 499
 |||
 Db 342 ESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLKKYVR 401
 Qy 500 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQ 559
 |||
 Db 402 AEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQ 461
 Qy 560 DEV 562
 |||
 Db 462 DEV 464

RESULT 7

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, D.C.

Biochemistry 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a multigene family.

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
 R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.

submitted to the EMBL Data Library, April 1993

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor like protein.

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.;
Hyman, B.T.; Neve, R.L.; Tanzi, R.E.
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the
Alzheimer's associated amyloid beta protein precursor.
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.8%; Score 1981.5; DB 2; Length 763;
Best Local Similarity 50.4%; Pred. No. 9.7e-99;
Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

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QY      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
      | ||| | || | : ||| : ||||| ||||| : ||| : ||| : |||
Db      15 LLLLLLVGLTAPALALAGYIEALANAGTGFVAEFPQIAMFCGKLNMHVNIQTGKWEPDF 74

QY      57 SGTKTCIDTKEGILQYQCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      : ||| : ||| : ||||| : ||||| : ||| : ||| : ||| : ||| : |||
Db      75 TGTKSCFETKEEVLYQCQEMYPQLQITNVMEANQVRSIDNWCRRDKKQCKS--RFVTPFK 132

QY      117 CLVGEFVSDALLVDPKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      ||||| ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      133 CLVGEFVSDVLLVPEKQCFHFKERMEVCENHQHWHHTVVKEACLTQGMTLYSYGMLLPCGV 192

QY      177 DKFRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAE 236
      | : | | : ||| : : | : ||| : : | | | : | | :
Db      193 DQFHGTEYVCCPQTKIIGSVSKEEEEEDEE-----EEEEDEEEDYDVYKSEFPTEAD 245

QY      237 VEE--EEA--DDDEDDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTESVE 284
      : | : | : |||| : ||| : : : | | | : | : :
Db      246 LEDFTEAAVDEDDDEEEGEEVVEDRDYYYDTFKGDDYNE--ENPTEPGSDGTMSDKEIT 303

QY      285 EVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVAVCGSA 344
      | : ||| : ||||| : ||||| : ||| | ||||| ||||| : ||||| :
Db      304 HDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVAVCKAM 363

QY      345 MSQSLLKTTQEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRE 404
      : | | | : || | | : ||| ||||| : ||| : |||
Db      364 I-----PPTPLPT-----NDVDVYFETSADDNEHARFQAKEQLEIRHRN 403

QY      405 RMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAM 464
      || : | : ||||| ||||| : : : ||||| | : ||| : ||| : ||||| : |||||

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Db 404 RMDRVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAM 463

QY 465 LNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
 |||||:||||: |||: |||| : |::||| ||| ||::||: |||: |||

Db 464 LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAA 523

QY 525 QIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEP 584
 |::||| || || ||||| || ||:|::|:|:|:|:|:|:|:|:|:|

Db 524 QMKSQVMTHLVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM----- 572

QY 585 RISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARP 644
 | |::| | | | |::|:| | | | | | | | | | | | | | | |

Db 573 -----DQFTASISETPVDVR---VSSEES-EEIPPFHPF--HPFPALPENE----DTQP 616

QY 645 AADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVG 696
 : : |||: | || |::| | | | |::|:| | | | | | | | | |

Db 617 ELYHPM--KKGSGVGEQDGGGLIGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVG 672

QY 697 S-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVD 739
 : |::|:| | |||||:|:|:|:|:|:|:|:|:|:|:|:|

Db 673 GLEERESVGPLREDFSLSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVD 732

QY 740 AAVTPEERHLSKMQQNGYENPTYKFFEQMQ 769
 :|||:|:|:|:|:|:|:|:|:|:|:|:|

Db 733 PMLTPEERHLNKMQNHYENPTYKYLEQMQ 762

RESULT 8

S42880

amyloid precursor-like protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999

C;Accession: S42880; S47528

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 submitted to the EMBL Data Library, March 1994

A;Description: Complete nucleotide and deduced amino acid sequence of rat amyloid precursor-like protein 2 (Aplp2/Apph): Two amino acids length difference to human and murine homologues.

A;Reference number: S42880

A;Accession: S42880

A;Molecule type: mRNA

A;Residues: 1-765 <SAN>

A;Cross-references: EMBL:X77934

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 Biochim. Biophys. Acta 1219, 167-170, 1994

A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor-like protein 2 (APLP2/APPH): two amino acids length difference to human and murine homologues.

A;Reference number: S47528; MUID:94368849; PMID:8086458

A;Accession: S47528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-765 <SA2>

A;Cross-references: EMBL:X77934

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.6%; Score 1971.5; DB 2; Length 765;
Best Local Similarity 49.7%; Pred. No. 3.3e-98;
Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

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QY      5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWSDP 56
      | :|||  || | :      |||  :|||||||:||||:| | ||: ||
Db      15 LLVLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGWEPDP 74

QY      57 SGTCTCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :|||:| | || :|||||:|||||:||||| | :||:| :|||:| | |||:|
Db      75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK 132

QY     117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
      ||||| ||| |||: | | ||||:| | | ||| | | | : | : |||||:|
Db     133 CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV 192

QY     177 DKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYA-DGSEDKVVVEAESEE 233
      | :| | | :||| | : :||: | : ||: : : : ||| | || | :
Db     193 DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEE-----DEEDYALDKSEFPTEADLEDT 248

QY     234 VAEVEEEEADDDDEDEDGDEVEEEAEPEYEE-----ATERTTSIATTTTTTTESVEEVV 287
      | :| :| :| :| :| :| | : : | : | | :| :| :| :| :|
Db     249 EAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKGDDYNEENPTEPSSDGTISDKIEAHDV 308

QY     288 REVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQ 347
      : |||:| | ||||:| : ||||:| ||| | ||||| ||||:| : ||||| : :
Db     309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNFESEDYCMVCKTMI-- 366

QY     348 SLKTTQEPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMS 407
      | ||| : || | || | :||| |||||:| | ||| :| | ||
Db     367 -----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRSRMD 408

QY     408 QVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLND 467
      :| :||| ||| |||||:| : |||| | :||:| | :| :|||:| :||| |||
Db     409 RVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLND 468

QY     468 RRRALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIR 527
      |||:||||: |||: ||| : | :||| ||| |||:| :| | |||:| :|
Db     469 RRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMK 528

QY     528 SQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDVLNMISEPRIS 587
      ||||| || || ||||| || |||:| :| :|||:| :|
Db     529 SQVMTHLVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM----- 574

QY     588 YGNDALMPSLTETKTTVELLPVNGEFSLLDLPWHSFGADSVANTENEVEPVDPARPAAD 647
      | | :| | | :| | :| :| | | :| :| | | :|
Db     575 ---DQFTSSISENPVDVR---VSSEES-EEIPPFHPF--HPFPSLSENE----DTQPELY 621

QY     648 RGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVEFFAEDVGS-- 697
      : : |||: | || | : ||| | :| :| :| | || |
Db     622 HPM--KKGSGMAEQDGGGLIGAEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLE 677

QY     698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVDAAV 742
      : | :|||:| | |||||:| |||:| :| | :| :|
Db     678 EEPDSVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPML 737
```

Qy 743 TPEERHLSKMQQNGYENPTYKFFEQMQ 769
 |||||:| :|||: |||
 Db 738 TPEERHLNKMQNNGYENPTYKYLEQMQ 764

RESULT 9

A49974
 beta-amyloid precursor protein 2 homolog APLP2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C;Accession: A49974
 R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
 J. Biol. Chem. 269, 2637-2644, 1994
 A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid precursor protein (APP).
 A;Reference number: A49974; MUID:94132029; PMID:8300594
 A;Accession: A49974
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-751 <SLU>
 A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
 A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
 F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.2%; Score 1956.5; DB 2; Length 751;
 Best Local Similarity 49.3%; Pred. No. 2.1e-97;
 Matches 397; Conservative 130; Mismatches 169; Indels 109; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
 | :||| || | : ||| :|||:|||||:||||:| ||: ||
 Db 15 LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPD 74
 Qy 57 SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
 :|||:| :|| :|||:|||||:||||| :||| :||| :|||: | |||:
 Db 75 TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132
 Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
 ||||| |||| | :| ||||:||| | ||| : || | : ||| |||||:
 Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192
 Qy 177 DKFRGVFVCCPLAE--ESDNVDSADAEEEDSDVWGGADTDYADGSEDKVVEVAE---E 231
 | :| | :||| : :||| | : ||| : | | || : :| |
 Db 193 DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLKSEFPTE 243
 Qy 232 EEVAEEVEEEAD-DEDEDGDEVEEEAE-----EPYEEATERTTTSIATTTTTTTTES 282
 : : | || :|||:| :| : : | | | | : : | : :
 Db 244 ADLEDFTAAADEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDKE 301
 Qy 283 VEEVREVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCG 342
 : | : |||:| |||||: |||||: ||| | |||||:| :|||
 Db 302 IVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCK 361
 Qy 343 SAMSQSLLKTTQEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKH 402

```

      : :      | |||      : || | || | : |||| | ||||: || :|
Db      362 AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH 401
Qy      403 RERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVE 462
      | || :| : |||| | ||||| : : : |||| | : ||||: ||||: ||||
Db      402 RNRMDRVKKEWEEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVE 461
Qy      463 AMLNDRRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPPK 522
      | ||||| : ||||: |||: ||| : | : |||| | || | || : ||: || | |||: |
Db      462 AMLNDRRRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEK 521
Qy      523 AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQEQNYSDDVLANMIS 582
      ||| : || |||| | || | || |||| | || ||||: ||||: || : |
Db      522 AAQMKSQVMTHLHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-- 572
Qy      583 EPRISYGN DALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDA 642
      | | : | | : | : | | | | : : |||
Db      573 -----DQFTSSISENPVDVRVSSEESE-EIPPFHPLHPF-----PSLSENE----- 612
Qy      643 RPAADRGLTTRPGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---- 697
      | : : | || : : | | : || | : | : || | || |
Db      613 ----GSGMAEQDG-GLIGAEKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEE 665
Qy      698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVEVDAAVTP 744
      : | : |||: | | ||||| : ||||: || : | | |||| : ||
Db      666 PESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTP 725
Qy      745 EERHLSKMQQNGYENPTYKFFEQMQ 769
      ||||| : ||| : ||||| ||| : ||||
Db      726 EERHLNKMQN HGYENPTYKYLEQMQ 750

```

RESULT 10

A46362

amyloid precursor-like protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C;Accession: A46362

R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992

A;Title: Identification of a mouse brain cDNA that encodes a protein related to
the Alzheimer disease-associated amyloid beta protein precursor.

A;Reference number: A46362; MUID:93066322; PMID:1279693

A;Accession: A46362

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-653 <WAS>

A;Experimental source: brain

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIIP:118684)

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology

C;Keywords: transmembrane protein

Query Match 28.4%; Score 1150.5; DB 2; Length 653;

Best Local Similarity 35.4%; Pred. No. 2.6e-54;

Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

Qy 1 MLPLGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRILNMHNMNVQNGKWDSDPSGT 59
 :|| :||| | | : | :| ||| :| :: :|: || :
 Db 22 LLP-LSLLLLRAQLAVGNLAVGSPSAEAPGSAQVAGLCGRLLTLHRDLRTGRWEPDPQRS 80

Qy 60 KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL 118
 :|: : :|:|:|:| | | :| | : : | | | | :|: ||
 Db 81 RRCLLDPQRVLEYCRQMYPELHIARVEQAAQAI PMERWCGGTRSGRCAHPHHEVVPFHCL 140

Qy 119 VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDK 178
 ||||:||||: :|:|:| | | :| | | : | | ||||| :|
 Db 141 PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEAQSSQGLILHSGMMLPCGSDR 200

Qy 179 FRGVEFVCCPLAEESDNVDSADAEEDDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV 237
 ||||:|||| : | | : : | | | :| | | ||||
 Db 201 FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-----EEEVESF 248

Qy 238 EEEEEADDEDEDEGDEVEEEAEPEYEATERTTTSIATTTTTTTESVEEVVREVCSEQAET 297
 : | : :| || | : |
 Db 249 PQPVDDYFVEPPQAESEEEEEERAPPPSSHTP----- 281

Qy 298 GPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPL 357
 |:|| ||
 Db 282 ----VMVSR----VT----- 288

Qy 358 ARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAE 417
 | || | || | ||: || | :|| || : ::||| | :
 Db 289 ---PTPRPT-----DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMAD 339

Qy 418 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 477
 |:|||||:|: :|| :||:|: : ||:|||| | | |:|:| | || : :
 Db 340 SQSKNLPKADRQALNEHFQSILQTLQVSGERQRLVETHATRVIALINDQRRAALEGFL 399

Qy 478 TALQAVPPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 537
 ||| ||: | | :|:|:|:|:|:|:|:|:| | ||:| | :| | |||:| |
 Db 400 AALQGDPPQAEVRLMALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRQVQVQTHLQVI 459

Qy 538 YERMNQSLSLYNVPAVAEEIQDEVDELLQKEQNYSDDVLANMISEPRISYGNALMP-S 596
 ||||| || | :|:|: : ||| || : : || :| |
 Db 460 EERMNQSLGLLDQNPHLAQELRPQIQELL-----LAEHLGPSEL----DASVPGS 505

Qy 597 LTETKTTVELLPVNGEFLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS 656
 :| | ||| | :|:| | :| | : |
 Db 506 SSEDK-----GSLQP-----PESKDDPPVTLP---KGSTDQESS 536

Qy 657 GLTNIKTEEISEVKMDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIA 713
 | : : : | : | | : : | :|:|
 Db 537 SSGREKLTPLEQYEQVNASAPRGFPFHSSDIQRDELAPSGTGVSREALSGLLIMGAGGG 596

Qy 714 TVIVITLVML-KKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 767
 :|:|:|:| | | | :| | ||||| :| | :| :|:|:|:|:| | :|
 Db 597 SLIVLSLLLLRKKKPYGTISHGVVEVDPMLTLEEQQRLRELQRHGYENPTYRFLEE 651

RESULT 11

JC1404

CDEI-box DNA-binding protein - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 C;Accession: JC1404
 R;Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A;Title: A murine sequence-specific DNA binding protein shows extensive local similarities to the amyloid precursor protein.
 A;Reference number: JC1404; MUID:93129193; PMID:1482349
 A;Accession: JC1404
 A;Molecule type: mRNA
 A;Residues: 1-511 <VID>
 C;Comment: This protein plays an important role in the early development of the mouse.
 C;Keywords: DNA binding; transmembrane protein

Query Match 27.4%; Score 1112.5; DB 2; Length 511;
 Best Local Similarity 43.0%; Pred. No. 2.1e-52;
 Matches 264; Conservative 87; Mismatches 136; Indels 127; Gaps 21;

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QY      174 CGIDKFRGVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEE 233
          ||::| | |::||| :: ||| | : | |||
Db      6  CGVDQFHGTEYVCCP---QTKTVDS-----DSTMSK-----EEEE 37

QY      234 VAEVEEEEEADDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSE 293
          |||: :|::| | |: | | :| | : | | ||| :
Db      38 ----EEDEEEDEEEDYDLKSEFPTEADLEDFTE---AAADEEEEEDEEEGEEVVED---- 86

QY      294 QAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTT 353
          :|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      87 -----RDYYD-----PF----KGDDYNEENPTE-----PSSEGTI--S 114

QY      354 QEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREW 413
          : : | ||:| | | | | | | | | | | | | | | | | | | | | | | |
Db      115 DKEIVHD-VKVPPTPLPTND-VDVYFETSADDNEHARFQKAKEQLEIRHRNRMDRVKKEW 172

QY      414 EEAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLAL 473
          |||| ||||| |:: :||| | |::|::|::|::|::|::|::|::|::|::|::|
Db      173 EEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRLAL 232

QY      474 ENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTH 533
          |||: |||: ||| : |::| | | |::|::| | |::|::|::|::|::|::|
Db      233 ENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTH 292

QY      534 LRVIYERMNQSLSLLYNPAVAEEIQDEVDELLQEQNYSDVLNMISEPRISYGN DAL 593
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      293 LHVIEERNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-----DQF 335

QY      594 MPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTR 653
          |::| | : | : | | | | : : || | : :
Db      336 TSSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE-----GSGMAEQ 379

QY      654 PGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKL VFFAEDVGS----- 697
          | | : : | | : || | : | :::| | | |
Db      380 DG-GLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAERVGGLEEEPE SVGPLREDF 436

QY      698 --NKGAIIGLMVGGVVIATVIVITLVM LKKKQYTSIHG VVEVDAAVTPEERHLSKMQQN 755
          : |::|:| | | | | | | | | | | | | | | | | | | | | | :

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Db 437 SLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNH 496
 QY 756 GYENPTYKFFEQMQ 769
 |||||: ||||
 Db 497 GYENPTYKYLEQMQ 510

RESULT 12

T15795

hypothetical protein C42D8.8 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
 C;Accession: T15795; A49414
 R;Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A;Description: The sequence of *C. elegans* cosmid C42D8.
 A;Reference number: Z18405
 A;Accession: T15795
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-686 <HAL>
 A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1;
 GSPDB:GN00028; CESP:C42D8.8
 A;Experimental source: strain Bristol N2; clone C42D8
 R;Daigle, I.; Li, C.
 Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
 A;Title: apl-1, a *Caenorhabditis elegans* gene encoding a protein related to the
 human beta-amyloid protein precursor.
 A;Reference number: A49414; MUID:94089766; PMID:8265668
 A;Accession: A49414
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 7-686 <DAI>
 A;Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
 C;Genetics:
 A;Gene: CESP:C42D8.8
 A;Map position: X
 A;Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3;
 580/3
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
 proteinase inhibitor homology

Query Match 19.3%; Score 785; DB 2; Length 686;
 Best Local Similarity 26.8%; Pred. No. 1.1e-34;
 Matches 224; Conservative 111; Mismatches 272; Indels 230; Gaps 23;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
 :: || : :| | | | | :| || | :| | :|
 Db 6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63
 QY 61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
 || | ||:|:| : || : |||:| : | :| :| : || | | || | : |
 Db 64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122
 QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLPC 174
 || | :| || | :| | | : || | : | | : : :| ||
 Db 123 EFHSEALQVPHDCQFSHVNSRDQCNDYQHWKDEAGQCKTKKSKGNKDMIVRSFAVLEPC 182

A;Accession: A32758
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-886 <ROS>
 A;Cross-references: GB:J04516; NID:g158371; PID:g158372
 C;Genetics:
 A;Gene: FlyBase:Appl
 A;Cross-references: FlyBase:FBgn0000108
 C;Keywords: transmembrane protein

Query Match 18.2%; Score 737.5; DB 2; Length 886;
 Best Local Similarity 24.7%; Pred. No. 5.2e-32;
 Matches 235; Conservative 137; Mismatches 313; Indels 265; Gaps 30;

QY	7	LLLLAAWTARALEVPTDGNAGLLA-----EPQIAMFC--GRINMHMNV-QNGKWDSDPSG	58
		: : : : : : : : : :	
Db	9	LLRLSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWVTDLSK	63
QY	59	T---KTCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRG---RKQCKTHPHFV	112
		: : : : : : : : : :	
Db	64	KTTGPTCLRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQALNAACKGSHRWI	123
QY	113	IPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMML	172
		: : : : : :	
Db	124	KPFRCL-GPFQSDALLVPEGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRTFAMLL	182
QY	173	PCGIDKFRGVEFVCCP-----LAESDNVD---SA	199
		: : :	
Db	183	PCGISVFSGVFVCCPKHFKTDEIHVKKTDLVMPAAQINSANDELMNDEDDSDNSNYSK	242
QY	200	DAEEDDSDVWVGADTDYADGSEDKVVEVAEEEEV-----AEV	237
		: : : :	
Db	243	DANEDDL-----DEDDLMGDDEEDDMVADEAATAGGSPNTGSSGDSNSGSLDDINAAY	296
QY	238	EE-EEADDDDEDGDEVEEEAEPEYEEA-TERTTSIATTTTTTTSVEEVVREVCSEQA	295
		: : : : : : : : : : : : :	
Db	297	DSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVVSLKSDSSSPSSAPVAPAPEKAPVKS	356
QY	296	ETGPCRAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQE	355
		: : : : : : : : :	
Db	357	ESVTSTPQLS-----ASAAAFVAANSNGSGT-----GAGAPPSTAQPTSD	396
QY	356	PLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEE	415
		: : : : : : : : : :	
Db	397	P-----YFTHFDPHYEHQSYKVSQKRLEESHREKVTRVMKDWS	435
QY	416	AERQAKNLPKADKKA-----VIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDR	468
		: : : : : : : : : :	
Db	436	LEEKYQDMRLADPKAAQSFQRMRTARFQTSVQALEEEGNAEKHQLAAMHQQRVLAHINQR	495
QY	469	RRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEH-VRMVDP---KKA	524
		: : : : : : : : : :	
Db	496	KREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRAHALAHYRHLNLSGGPGGLEAAA	555
QY	525	QIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEI-----QDEV-----	562
		: : : : : : : : :	
Db	556	SERPRTLRLIDIDRAVNQSMTMLKRYPELSAKIAQLMNDYILALRSKDDIPGSSSLGMSE	615

Qy 563 -----DELLQKEQNYSDDVLAN 579
 Db 616 EAEAGILDKYRVEIERKVAEKERLRLAEKQKQRAAEREKLRLEAKKVDDMLKS 675
 Qy 580 MISE-----PRISYGNDAIM-----PSLTETKTTVELLPVNG 611
 Db 676 QVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDAAALVTAANPNLETTKS----- 726
 Qy 612 EFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKM 671
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RESULT 14

S38344

CDEI-binding protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996

C;Accession: S38344

R;Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.

Biochim. Biophys. Acta 1216, 154-156, 1993

A;Title: The complete cDNA coding sequence for the mouse CDEI binding protein.

A;Reference number: S38344; MUID:94032480; PMID:8218408

A;Accession: S38344

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-246 <HAN>

A;Cross-references: EMBL:Z22592

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 17.4%; Score 706; DB 2; Length 246;

Best Local Similarity 51.5%; Pred. No. 5e-31;

Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

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 Qy 57 SGTKTCTIDTKEGILQYQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:15:49 ; Search time 144.786 Seconds
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1669.522 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1292805

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result
No. Score Match Length DB ID Description

1	4058	100.0	770	9	US-09-794-927-55	Sequence 55, Appl
2	4058	100.0	770	9	US-09-795-847-55	Sequence 55, Appl
3	4058	100.0	770	9	US-09-794-743-55	Sequence 55, Appl
4	4058	100.0	770	9	US-09-794-748-55	Sequence 55, Appl
5	4058	100.0	770	9	US-09-904-987-2	Sequence 2, Appli
6	4058	100.0	770	9	US-09-794-925-55	Sequence 55, Appl
7	4058	100.0	770	9	US-09-681-442-55	Sequence 55, Appl
8	4058	100.0	770	9	US-09-149-718-6	Sequence 6, Appli
9	4058	100.0	770	9	US-09-785-215-2	Sequence 2, Appli
10	4058	100.0	770	10	US-09-848-616-172	Sequence 172, App
11	4058	100.0	770	10	US-09-869-414-55	Sequence 55, Appl
12	4058	100.0	770	10	US-09-548-366-55	Sequence 55, Appl
13	4058	100.0	770	12	US-10-652-927-55	Sequence 55, Appl
14	4058	100.0	770	12	US-10-652-830-55	Sequence 55, Appl
15	4058	100.0	770	14	US-10-217-584-5	Sequence 5, Appli
16	4058	100.0	770	14	US-10-204-362-2	Sequence 2, Appli
17	4058	100.0	770	14	US-10-169-580-5	Sequence 5, Appli
18	4058	100.0	770	14	US-10-335-035-3	Sequence 3, Appli
19	4058	100.0	770	14	US-10-223-809A-2	Sequence 2, Appli
20	4058	100.0	770	14	US-10-010-942B-38	Sequence 38, Appl
21	4058	100.0	770	14	US-10-357-935-3	Sequence 3, Appli
22	4058	100.0	770	14	US-10-050-902-218	Sequence 218, App
23	4058	100.0	770	14	US-10-050-898-218	Sequence 218, App
24	4058	100.0	770	15	US-10-427-208-75	Sequence 75, Appl
25	4058	100.0	770	15	US-10-428-487-12	Sequence 12, Appl
26	4058	100.0	770	16	US-10-388-389-38	Sequence 38, Appl
27	4058	100.0	770	16	US-10-281-092-10	Sequence 10, Appl
28	4058	100.0	770	16	US-10-622-087-92	Sequence 92, Appl
29	4058	100.0	772	9	US-09-794-927-59	Sequence 59, Appl
30	4058	100.0	772	9	US-09-795-847-59	Sequence 59, Appl
31	4058	100.0	772	9	US-09-794-743-59	Sequence 59, Appl
32	4058	100.0	772	9	US-09-794-748-59	Sequence 59, Appl
33	4058	100.0	772	9	US-09-794-925-59	Sequence 59, Appl
34	4058	100.0	772	9	US-09-681-442-59	Sequence 59, Appl
35	4058	100.0	772	10	US-09-869-414-59	Sequence 59, Appl
36	4058	100.0	772	10	US-09-548-366-59	Sequence 59, Appl
37	4058	100.0	772	12	US-10-652-927-59	Sequence 59, Appl
38	4058	100.0	772	12	US-10-652-830-59	Sequence 59, Appl
39	3943.5	97.2	751	9	US-09-794-927-57	Sequence 57, Appl
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42	3943.5	97.2	751	9	US-09-794-748-57	Sequence 57, Appl
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44	3943.5	97.2	751	9	US-09-681-442-57	Sequence 57, Appl
45	3943.5	97.2	751	9	US-09-149-718-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-794-927-55

; Sequence 55, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-55

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Query Match          100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-795-847-55

; Sequence 55, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-794-748-55

; Sequence 55, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
QY	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEEE	240
QY	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
QY	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
QY	361	PVKLPPTTAASTPDAVDKYLETPGDENHAHFQAKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENHAHFQAKAKERLEAKHRERMSQVMREWEAAERQA	420
QY	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
QY	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540

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Db      481  |||||QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
QY      541  MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET 600
Db      541  |||||MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTET 600
QY      601  KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db      601  |||||KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
QY      661  IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Db      661  |||||IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
QY      721  VMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN 770
Db      721  |||||VMLKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN 770

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RESULT 5

US-09-904-987-2

; Sequence 2, Application US/09904987

; Patent No. US20020037908A1

; GENERAL INFORMATION:

; APPLICANT: No. US20020037908A1actyl, Inc.

; TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathological

; TITLE OF INVENTION: Protein Assembly or Aggregation

; FILE REFERENCE: 42108/26146

; CURRENT APPLICATION NUMBER: US/09/904,987

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 770

; TYPE: PRT

; ORGANISM: homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4

; DATABASE ENTRY DATE: 2000-09-15

; RELEVANT RESIDUES: (1)..(770)

US-09-904-987-2

Query Match 100.0%; Score 4058; DB 9; Length 770;

Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
Db      1  |||||MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
QY      61  TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db      61  |||||TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
QY      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

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Db	121		EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181		GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181		GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241		EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241		EADDDDEDEDGDEVEEEAEEPVEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301		RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301		RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361		PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361		PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421		KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541		MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541		MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601		KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601		KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721		VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721		VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

RESULT 6

US-09-794-925-55

; Sequence 55, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

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; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-55
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Query Match          100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MLPGIALLLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGIALLLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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QY 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
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 Db 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 QY 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTET 600
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 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNLMPSLTET 600
 QY 601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
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 Db 601 KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 QY 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 7

US-09-681-442-55

; Sequence 55, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-681-442-55

Query Match 100.0%; Score 4058; DB 9; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLPG LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
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Db      1 MLPG LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60

QY     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

QY    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY    181 GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
      |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240

QY    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
      |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

QY    301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      |||
Db    301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

QY    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
      |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

QY    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
      |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

QY    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
      |||
Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

QY    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
      |||
Db    541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600

QY    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
      |||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660

QY    661 IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
      |||
Db    661 IKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

QY    721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
      |||
Db    721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
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RESULT 8
US-09-149-718-6

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; Sequence 6, Application US/09149718
; Patent No. US20020104104A1
; GENERAL INFORMATION:
;   APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
;   APPLICANT: Peter A. Seubert, and Russell E. Rydel
;   TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
;   TITLE OF INVENTION: Therapeutics Using Transgenic Animal Models
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: 2800 One Atlantic Center
;     STREET: 1201 West Peachtree Street
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-3450
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/149,718
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/660,487
;     FILING DATE:
;     APPLICATION NUMBER: 08/480,653
;     FILING DATE: June 7, 1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: ANS101CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404)-873-8794
;     TELEFAX: (404)-873-8795
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 770 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-149-718-6

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Query Match          100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

QY     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120

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Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDGDEVEEEAAEPYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDGDEVEEEAAEPYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN	770

RESULT 9

US-09-785-215-2

; Sequence 2, Application US/09785215

; Publication No. US20020187157A1

; GENERAL INFORMATION:

; APPLICANT: JENSEN, Martin Roland et al.

; TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID

; FILE REFERENCE: 3631-0107P

; CURRENT APPLICATION NUMBER: US/09/785,215

; CURRENT FILING DATE: 2001-02-20

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-215-2

Query Match 100.0%; Score 4058; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Db	241	EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDAIMPSLTET	600
Db	541	MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDAIMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 VMLKKKOYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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Db      361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
Qy      421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Qy      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Db      481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      541 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
Db      541 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
Qy      601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db      601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQQMN 770
Db      721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQQMN 770

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RESULT 11

US-09-869-414-55

; Sequence 55, Application US/09869414

; Publication No. US20030077226A1

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-869-414-55

Query Match 100.0%; Score 4058; DB 10; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEQDEVDLLOKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEQDEVDLLOKEQNYSDVLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770

US-09-548-366-55

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES THEREFOR

FILE REFERENCE: 28341/6280A

7 CURRENT APPLICATION NUMBER: US/09/548,366

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-548-366-55

Query Match 100.0%; Score 4058; DB 10; Length 770;

Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVONGKWDSDPSGK 60

Qy 61 TCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
| | | | |

Db 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIONWCKRGRKOCKTHPHFVIPYRCLVG 120

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

[illegible]

Db 181 GVEFVCCPLAEESDNVDSADAEEDDSDVWGGADTDYADGSEDPKVEVAEEEEVAEVEEE 240

[illegible]

Db 241 EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTTESVEEVVREVCSEOETGPC 300

Qy 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
 |||||
 Db 301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
 |||||
 Qy 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
 |||||
 Db 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
 |||||
 Qy 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
 |||||
 Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
 |||||
 Qy 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||||
 Db 481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 |||||
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
 |||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET 600
 |||||
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 |||||
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||||
 Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
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RESULT 13

US-10-652-927-55

; Sequence 55, Application US/10652927

; Publication No. US20040043408A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N3

; CURRENT APPLICATION NUMBER: US/10/652,927

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-927-55

Query Match 100.0%; Score 4058; DB 12; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNLALMPSLTET	600
Qy	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720

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Db          661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy          721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770
Db          721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770

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RESULT 14

US-10-652-830-55

; Sequence 55, Application US/10652830

; Publication No. US20040048303A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N1

; CURRENT APPLICATION NUMBER: US/10/652,830

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-652-830-55

Query Match 100.0%; Score 4058; DB 12; Length 770;

Best Local Similarity 100.0%; Pred. No. 2.4e-257;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
Db          1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK 60
Qy          61 TCIDTKEGILQYQCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Db          61 TCIDTKEGILQYQCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
Qy          121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db          121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy          181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

```

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Db      181  |||||GVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEEEEVAEVEEE 240
Qy      241  EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
Db      241  |||||EADDDDEDDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
Qy      301  RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
Db      301  |||||RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
Qy      361  PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
Db      361  |||||PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
Qy      421  KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db      421  |||||KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Qy      481  QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Db      481  |||||QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      541  MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Db      541  |||||MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
Qy      601  KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db      601  |||||KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      661  IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Db      661  |||||IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      721  VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db      721  |||||VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 15

US-10-217-584-5

; Sequence 5, Application US/10217584

; Publication No. US20030077261A1

; GENERAL INFORMATION:

; APPLICANT: Paris, Daniel

; APPLICANT: Mullan, Michael

; TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides

; FILE REFERENCE: USF-T161XC1

; CURRENT APPLICATION NUMBER: US/10/217,584

; CURRENT FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: 60/311,656

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 770

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(770)
; OTHER INFORMATION: Amyloid precursor protein
US-10-217-584-5
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Query Match          100.0%; Score 4058; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
        |||
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120
        |||
Db     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||
Db    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
        |||
Db    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        |||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360

Qy    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420
        |||
Db    361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITAL 480
        |||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAAENERQQLVETHMARVEAMLNDRRRLALENYITAL 480

Qy    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
        |||
Db    481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540

Qy    541 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
        |||
Db    541 MNQSLSLLYNVPAAVAEEIQDEVDLLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600

Qy    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTN 660
        |||
Db    601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGLTN 660

Qy    661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
```

Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720

Qy 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

Db 721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

Search completed: August 13, 2004, 09:33:23

Job time : 147.786 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:53 ; Search time 117.521 Seconds
(without alignments)
2067.275 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	3719.5	91.7	751	13	Q9DGJ7	Q9dgj7	gallus gall
2	3403.5	83.9	747	13	Q91963	Q91963	xenopus. ap
3	3377.5	83.2	695	13	Q9DGJ8	Q9dgj8	gallus gall
4	3163.5	78.0	693	13	Q98SG0	Q98sg0	xenopus lae
5	3152.5	77.7	695	13	Q98SF9	Q98sf9	xenopus lae
6	3150.5	77.6	695	13	Q7ZXQ0	Q7zxq0	xenopus lae
7	2914	71.8	699	13	O57394	O57394	narke japon
8	2785.5	68.6	738	13	Q90W28	Q90w28	brachydanio
9	2717	67.0	569	13	Q9PVL1	Q9pvl1	gallus gall
10	2562.5	63.1	534	13	O93296	O93296	gallus gall
11	2516.5	62.0	678	13	Q7ZZT1	Q7zzt1	brachydanio
12	2437	60.1	694	13	Q8UUR9	Q8uur9	brachydanio
13	2288.5	56.4	612	13	Q9I9E7	Q9i9e7	brachydanio
14	1960.5	48.3	763	11	Q61482	Q61482	mus musculu
15	1956.5	48.2	751	11	Q60709	Q60709	mus musculu
16	1928	47.5	384	11	Q8BPC7	Q8bpc7	mus musculu
17	1733.5	42.7	695	4	Q13861	Q13861	homo sapien
18	1721	42.4	669	4	Q14662	Q14662	homo sapien
19	1713.5	42.2	707	11	Q80US7	Q80us7	mus musculu
20	1709.5	42.1	695	11	Q64348	Q64348	mus musculu
21	1700.5	41.9	715	11	Q7TT34	Q7tt34	mus musculu
22	1604.5	39.5	472	13	Q8UUS0	Q8uus0	brachydanio
23	1350.5	33.3	357	13	Q8UUI8	Q8uui8	brachydanio
24	1302	32.1	523	4	Q14594	Q14594	homo sapien
25	1267	31.2	522	4	Q9BT36	Q9bt36	homo sapien
26	1090	26.9	218	11	Q8BPV5	Q8bpv5	mus musculu
27	795	19.6	357	13	Q7ZZT2	Q7zzt2	brachydanio
28	788	19.4	160	11	Q9QZ78	Q9qz78	cavia sp. p
29	771	19.0	239	13	Q8UUI7	Q8uui7	brachydanio
30	577	14.2	113	13	Q8JH58	Q8jh58	chelydra se
31	561	13.8	182	11	Q9CYS4	Q9cys4	mus musculu
32	478	11.8	97	6	Q28673	Q28673	oryctolagus
33	435.5	10.7	140	13	Q800X9	Q800x9	chelydra se
34	393.5	9.7	82	4	Q16019	Q16019	homo sapien
35	389.5	9.6	82	4	Q16014	Q16014	homo sapien
36	387.5	9.5	82	4	Q16020	Q16020	homo sapien
37	376	9.3	79	11	O35463	O35463	cricketulus
38	335	8.3	208	11	Q8R0R7	Q8r0r7	mus musculu
39	282	6.9	82	13	Q7ZZT3	Q7zzt3	brachydanio
40	239	5.9	49	6	O97917	O97917	bos taurus
41	207	5.1	3198	5	Q9U8G8	Q9u8g8	manduca sex
42	205.5	5.1	759	5	Q8IT91	Q8it91	ancylostoma
43	194.5	4.8	2225	5	O45881	O45881	caenorhabdi
44	187	4.6	2772	5	Q9VAV4	Q9vav4	drosophila
45	187	4.6	2776	5	Q869A0	Q869a0	drosophila

ALIGNMENTS

RESULT 1

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF289219; AAG00594.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 91.7%; Score 3719.5; DB 13; Length 751;
 Best Local Similarity 91.7%; Pred. No. 6.9e-220;
 Matches 708; Conservative 18; Mismatches 23; Indels 23; Gaps 4;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPHLALLLLAAGAARALEVPADGNAGLLAEPQIAMFCGKLNHMNMNVQNGKWESDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGWKQCNGHPHIVVPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKLLHQERMDVCETHLHWHTVAKESCSEKSMNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVE--VAEEEEVAEVE	238
Db	181	GVEFVCCPLAEESDNLDSADAEDDDSDVWVGADADYADGSDDKVVEEQPEEDEELTVVE	240
Qy	239	EEEADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG	298
		: : : :	

DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLÖIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 83.9%; Score 3403.5; DB 13; Length 747;
 Best Local Similarity 85.2%; Pred. No. 1.7e-200;
 Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

Qy	17	ALEVPTDGNAGLLAEPQIAMF-CGRLNMHMNVQNGKWSDPSGKTCIDTKEGILQYCQE	75
		::	
Db	15	ALEVLVDGNGGLLAEPQIAMFSVARLNMHMNVQNGKWETDVSG---CIGTKEGILQYCQE	71
Qy	76	VYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKF	135
		: : :	
Db	72	VYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVGEFVSDALLVPDKCKF	131
Qy	136	LHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDN	195
		: : : : ::	
Db	132	LHQERMDICETHLHWHTVAKESCSEKSMSLHEYGMLLPCGIDKFRGVEFVCCPSAEES	191
Qy	196	VDSADAEEDSDVWVGADTDYADGSEDKVVEVA---EEEEVAEVEEEEADDDDEDDEDGDE	253
		:	
Db	192	FDSADAAEDDCDVWVGADADYVDRSDDKAVEAQPDDEEEVVEVEEETDDDED--DGDE	249
Qy	254	VEEEAEPEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPCRAMISRWFYDVTE	313
		:	
Db	250	AEEPEPEPYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETGPCRAMISRWYYDVTE	309
Qy	314	GKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLKTTQEPLARDPVKLPTTAASTPD	373
		::: :	
Db	310	SKCAQFIYGGCGGNRNNFESDDYCMVCGSV-----IPATAASTPD	350
Qy	374	AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAERQAKNLPKADKKAVIQ	433
		: : : :	
Db	351	AVDKYLENPNDENEHDFLKAKEKLEKHKREKMSQVMREWEAERQAKNLPKADKKAVIQ	410
Qy	434	HFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFN	493
		: :	
Db	411	HFQEKVESLEQEAQKQQLVETHMARVEAMLNDRRLALENYITALQADPPRPRHVFN	470

Qy	494	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVPA	553
Db	471	LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVINERMNQSFSLLYKVPA	530
Qy	554	VAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDAIMPSTTETKTTVELLPVNGEF	613
Db	531	VAEEIQDEVDELQKEQNYSDDMVSNMVS DHRVSYGNDAIMPSTTETKTTVELLPVDGEF	590
Qy	614	SLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDA	673
		:::	
Db	591	NIEDLQPWHSFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDS	650
Qy	674	EFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHH	733
		:: :	
Db	651	EYRHDTAYEVHHQKL VFFAEVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTTIHH	710
Qy	734	GVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	711	GVVEVDAAVTPEERHLTKMOONGYENPTYKFFEQMON	747

Q9DGJ8

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ID      Q9DGJ8      PRELIMINARY;      PRT;      695 AA.
AC      Q9DGJ8;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Beta-amyloid precursor protein 695 isoform.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sarasa M., Rodolosse A., Sorribas V.;
RT      "Cloning of full-length chicken beta-amyloid precursor protein
RT      isoforms.";
RL      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF289218; AAG00593.1; -.
DR      HSSP; P05067; 1BA4.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      SMART; SM00006; A4_EXTRA; 1.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
SQ      SEQUENCE      695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

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AC Q98SG0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -.
 DR HSSP; P05067; 1HZ3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 78.0%; Score 3163.5; DB 13; Length 693;
 Best Local Similarity 79.1%; Pred. No. 8e-186;
 Matches 611; Conservative 37; Mismatches 43; Indels 81; Gaps 5;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK 60
 ||| : ||:| | |||| ||| ||||| :||| :||| :|||
 Db 1 MLPHITLLVLTV-GALALEVPADGNGGLAEPQIAMFCGKLNMHMNVQNGKWETDVSGLK 59
 Qy 61 TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVPIPYRCLVG 120
 || ||||| :||| :||| :||| :||| :||| :||| :|||
 Db 60 GCIGTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG 119
 Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 ||||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKSMLEHYGMLLPCGIDKFR 179
 Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVA--EEEEVAEVE 238
 ||||| ||||: |||| |||| |||| || ||| :|| || |||| |||
 Db 180 GVEFVCCPSAESESFDSADA-EDSDAWVGADADYVDRSDDKAVEAQPDEEEVEVEVE 238
 Qy 239 EEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETG 298
 ||| |||| |||| ||| ||||| :||| :||| :||| :|||
 Db 239 EEETDDDED--DGDEAEPEPEYEEATERTTSIATTTTTTTESVEEVVR----- 286
 Qy 299 PCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLA 358

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ID      Q98SF9          PRELIMINARY;      PRT;      695 AA.
AC      Q98SF9;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Beta-amyloid precursor protein B.
GN      APP.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Van den Hurk W.H.;
RL      Thesis (2001), Department of Biological Sciences,
RL      University of Nijmegen, Nijmegen, Netherlands.
DR      EMBL; AJ298151; CAC37194.1; -.
DR      HSSP; P05067; 1HZ3.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.

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DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL          1          18          POTENTIAL.
SQ   SEQUENCE      695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

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Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK	59
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	60	GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG	119
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	120	EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSSEKIMSLHEYGMLLPCGIDKFR	179
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDYADGSEDKVVEV--AEEEEVAEVE	238
Db	180	GVEFVCCPTAEESSESFDSADA-EDDSDVWWGGADADYVDRSDDKAVEAQPEEEEEVVEVE	238
Qy	239	EEEEADDEDDEDGDEVEEEAAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEAETG	298
Db	239	EEEEADD-DEDDGDETEEEPEEPYEEATERTTSIATTTTTTTTESVEEVVRAV-----	289
Qy	299	PCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAMSQSLLKTTQEPLA	358
Db	290	-----	289
Qy	359	RDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAER	418
Db	290	-----PATAVSTPDAVDKYLENPNDENEHDFLAKAKERLEGKHREKMSEVMKEWEAAER	343
Qy	419	QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT	478
Db	344	QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRIALENYIT	403
Qy	479	ALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIY	538
Db	404	ALQADPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIN	463
Qy	539	ERMNQSLSLLYNVPAAVEEIQDEVDELLOKEQNYSDVLNMISEPRISYGNLMPSLT	598
Db	464	ERMNQSFSLLYKVPAAVEEIQDEVDELFOKEQNYSDMVSNMVSDHRVSYGNLMPSLS	523
Qy	599	ETKTTVELLPVNGEFSLDDLQPVHWSFGADSVPAANTENEVEPVDPARPAADRGLTTRPGSGL	658
Db	524	ETKTTVELLPVDGEFNVEDLQPVHWSFGVDSVPANTENEVEPVDPARPAADRGLTTRPGSGL	583

Qy	659	TNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV	IATVIVI	718
		: : : : : : :		
Db	584	TNIKREEISEVKMDSEYRHDAAEYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV	IATVIVI	643
Qy	719	TLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN		770
		: : : : : : :		
Db	644	TLVMLKKKQYTTIHGGVVEVDAAVTPEERHLTKMQONGYENPTYKFFEQMON		695

```
Q7ZXQ0
ID   Q7ZXQ0          PRELIMINARY;      PRT;    695 AA.
AC   Q7ZXQ0;
DT   01-JUN-2003   (TrEMBLrel. 24, Created)
DT   01-JUN-2003   (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003   (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC044324; AAH44324.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE      695 AA;  78803 MW;  C1BD8AACC3356B05 CRC64;
```

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK	60
		: : : :	
Db	1	MLPHITLLVLTA-GALALEVPADGNGGLLAEPQIAMFCGKLNMHMNVQNGKWETDVSGTK	59
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
		: : :	
Db	60	GCIGTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKKGRKQCKSRTHIVVPYRCLVG	119
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
		: : : :	
Db	120	EFVSDALLVPDKCKFLHQERMDICETHLHWHTVAKESCSEKIMSLHEYGMLLPCGIDKFR	179

Db 341 EWEEAERQAKNLPKADKKAVIQRFQEMVESLEQEASERQQLVETHMARVEAMLNDRRRI 400

Qy 472 ALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVM 531
 ||||: ||| ||||| | |||| ||||| |||||: ||| |||: |||||: ||||

Db 401 ALENYLAALQADPPRPRHVLNALKKYSRAEQKDRQHTLKHFDHVRVDPEKAAQIKSQVM 460

Qy 532 THLRVIYERMNQSLSLLYNVPAAVEEQDEVDPELLQKEQNYSDVLANMISEPRISYGND 591
 ||| || ||||| ||||| ||: ||||| |||||: ||: ||: ||| :|: |||||

Db 461 THLHVIDERMNQSLSLLYKVPSVAEEIQDEVDPELLQRERSYMDMMANSVSDTRISYGND 520

Qy 592 ALMPSLTETKTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLT 651
 ||: |||: |||||: |||| : ||| ||||| | | : ||: ||||| ||||| |||||

Db 521 ALVPSLSETKTTIELLPDDGEFILDDLQPPHPFVIESIPANTENEVEPVDARPAPDRGLT 580

Qy 652 TRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
 ||||| |||||: ||: ||: ||: ||||| ||||| : ||||| |||||

Db 581 TRPGSGLTGIKTEEIAELKMETEFQQDSGYEVHHQKLVFFPKDVGSNKGAIIGLMVGGVV 640

Qy 712 IATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 641 IATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 699

RESULT 8

Q90W28

ID Q90W28 PRELIMINARY; PRT; 738 AA.

AC Q90W28;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Amyloid precursor protein.

GN APPA OR APP.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Groth C., Lardelli M.;

RT "Expression analysis of zebrafish app.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF389401; AAK64495.1; -.

DR ZFIN; ZDB-GENE-000616-13; appa.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.

DR InterPro; IPR001255; Beta-APP.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

Query Match 68.6%; Score 2785.5; DB 13; Length 738;
Best Local Similarity 69.9%; Pred. No. 1.3e-162;
Matches 540; Conservative 85; Mismatches 101; Indels 47; Gaps 14;

Qy 5 LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHMNVQNGKWDSDPSGKTCID 64
| :||:| : |:||:| |||||:||||:|:|:|:| ||||:|:|
Db 6 LFILLMAVASTLAVEVPSDGTGLLAEPQIAMFCGKLNMHINIQSGKWEPPSGSKSCIG 65

Qy 65 TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVS 124
|||||:|||||:|||||:|:|:|:| ||||:| | |:|:|:|:|
Db 66 NKEGILQYCQEVYPELQITNVVEANQPSIWDWCKKSRKQCRSHMHIVPYRCLVGEFVS 125

Qy 125 DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF 184
|||||:|||||:|:|:|:|:|:|:| |||||:|:|:|:|:|:|
Db 126 DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF 185

Qy 185 VCCPLAEESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEEVEEEADD 244
||| | : :|| | |||||:| | : | : : | | :|:|:|:
Db 186 VCCP-ADAGKESESAAVEEDSDVWGGAEADYTENSMTR--DAAAEPAVLE-DDEDADE 241

Qy 245 DED-DEDGD-----EVEEEAEPEYEATERTT-SIATTTTTTTESVEEVVREVCSEQAET 297
:|| |:|| | :||| || || | : : : |||||:| ||| |||
Db 242 EEDEDQDGDGRDEKIEEEEE--EERTQSTSAALTSTTTTTTESVEEVVREVCFASAET 299

Qy 298 GPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPL 357
|||:|:|:| | :||| | |||||:|:|:|:|:|
Db 300 GPCRAMLSRWYYVREERRCAPFIYGGCGGNRNFESEYCLSVCSGV----- 346

Qy 358 ARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAE 417
||| :| | ||||:| || | ||||| ||| || | |||||:|
Db 347 -----LTPSSSPDPAVDRYLET PADENEHAHFLKAKESLETKHRERMSQVMREWEAE 400

Qy 418 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 477
|||:|:|:| | |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 401 RQAKSLPRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRLALESYL 460

Qy 478 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 537
:||| | |||||:|:|:|:|:|:|:| |||||:|:|:|:|
Db 461 SALQADPPRPRHVFSLLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVI 520

Qy 538 YERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSL 597
||| || | || :||:| ||||:| |||:| | :|:|:|:|
Db 521 EERMNQSLGLLYKVPGVADDIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDS 579

Qy 598 TETKTTVELLPVNGEFSLDDLQPVHWSFGADSVANTENEVEPVDPARPAADRGLTTRPGSG 657
| :||| | : | || || |:|:|:|:| | | ||| ||
Db 580 T---AGLELLPAEDTQGFQFIHP-ESFN---QPNTHNQVEPVDPARVPDLDLATRPVSG 631

Qy 658 LTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIV 717

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Db          632 L---KPDDIPELRMEAEERHS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIV 685
Qy          718 ITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db          686 ITLVMLRKKQYTSIHGGIIEVDAAVTPEERHLSKMOONGYENPTYKFFEOMHN 738

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RESULT 9

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Q9PVL1
ID   Q9PVL1          PRELIMINARY;          PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

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Query Match 67.0%; Score 2717; DB 13; Length 569;
Best Local Similarity 82.5%; Pred. No. 1.5e-158;
Matches 534; Conservative 15; Mismatches 18; Indels 80; Gaps 5;

[illegible]

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Db      121 DD-DDDDGDEI-EETEEEEEATERTTSIATTTTTTTSVEEVVR----- 163
Qy      304 ISRWYFDVTEGKCAPFFYGGCGGNRRNFDTEEYCMVCGSAMSQSLKTTQEPLARDPVK 363
Db      164 ----- 163
Qy      364 LPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNL 423
      :||||||| |||||||||||||||||||||||||||||||||||
Db      164 VPTTAASTPDVVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNL 223
Qy      424 PKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITALQAV 483
      ||||||||| |||||||||||||||||||:|||||||
Db      224 PKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRRLALENYITALQTV 283
Qy      484 PPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQ 543
      ||||||||| |||||||||||||||||||
Db      284 PPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAVQIRSQVMTHLRVIYERMNQ 343
Qy      544 SLSLLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPSLTETKTT 603
      ||| ||||||||| |||||||||||||||||||:|||||
Db      344 SLSFLYNVPAVAEEIQDEVDELLQKEQNYSDVLNMISEPRISYGN DALMPTLTETKTT 403
Qy      604 VELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNIKT 663
      ||||| ||||||| || |||||||||||||||||||:|
Db      404 VELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKT 463
Qy      664 EEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVML 723
      ||:||||||||| ||||||||| |||||||
Db      464 EEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVITLVML 523
Qy      724 KKKQYTSIHHGVVEVDAAVTP EERHLSKMQQNGYENPTYKFFEQM QN 770
      ||||||||| ||||||||| |||||||
Db      524 KKKQYTSIHHGVVEVDAAVTP-ERHLSKMQQNGYENPTYKFFEQM QN 569

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RESULT 10

O93296

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ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.

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Qy 762 YKFFEOMQN 770
 |||||
Db 526 YKFFEOMQN 534

RESULT 11

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Q7ZZT1
ID   Q7ZZT1          PRELIMINARY;          PRT;    678 AA.
AC   Q7ZZT1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid protein a variant 2.
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Investigation of zebrafish appa expression during embryogenesis.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY271746; AAP22958.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE    678 AA;  76755 MW;  94163778444FD0BC CRC64;

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Query Match 62.0%; Score 2516.5; DB 13; Length 678;
Best Local Similarity 64.8%; Pred. No. 3.9e-146;
Matches 498; Conservative 79; Mismatches 94; Indels 97; Gaps 12;

Qy	5	LALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGKTCTCID	64
Db	6	LFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSGSKSCIG	65
Qy	65	TKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIYRCLVGEFVS	124
Db	66	NKEGILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVS	125
Qy	125	DALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEF	184
Db	126	DALLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEF	185
Qy	185	VCCPLAEESDNVDSADAEEDDSDVVWGGADTDYADGSEDKVVEVAEEEEVAEEEEADD	244
Db	186	VCCP-ADAGKESESAAVEEDDSDVVWGGAEADYTENSMTR--DAAAEPV--LEDDEDAD	240

Qy 245 DEDDEDGD-EVEEEAEEPYEEATERTT-SIATTTTTTTESEVEEVVREVCSEQAETGPCRA 302
 :|:||||| : :|: || || |: |: :: :|:|||||
 Db 241 EEEDEDGDGRDEKIEEEEEERTQSTSAALTSTTTTTTESVEEVVR----- 286

Qy 303 MISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARDPV 362
 Db 287 ----- 286

Qy 363 KLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKN 422
 :|| :|:| ||||:|||| ||||| ||| || |||||:|||||:|
 Db 287 -VPTPSSSPDAVDRYLET PADENEHAHFLKAKESLETKHRERMSQVMREWEEAERQAKS 345

Qy 423 LPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITALQA 482
 ||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|:|
 Db 346 LPRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQA 405

Qy 483 VPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMN 542
 |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 406 DPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMN 465

Qy 543 QSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTETKT 602
 ||| ||| || ||:|:|:| ||||:| |||: |: |:|:|:|:|:| |
 Db 466 QSLGLLYKVPGVADDIQDQV-ELLQREQQEMSAQLANLQSDARVSYGNDALMPDST---A 521

Qy 603 TVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIK 662
 :||| : | || || |:|:|:|:| | | ||| ||| |
 Db 522 GLELLPAEDTQGFGEFHP-ESFN----QPNTHNQVEPVDARVPVLDLATRPVSGL---K 573

Qy 663 TEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVM 722
 :|:| |:|:| || ||:|:|:|:|:| |||||:|:|:|:|:|:|:|:|:|
 Db 574 PDDIPELRMEAEERHS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLVM 630

Qy 723 LKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 631 LRKKQYTSIHGGIIEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 678

RESULT 12

Q8UUR9

ID Q8UUR9 PRELIMINARY; PRT; 694 AA.
 AC Q8UUR9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative membrane protein.
 GN APPB.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=11862463;
 RA Musa A., Lehrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human

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RT APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315639; CAC85736.1; -.
DR ZFIN; ZDB-GENE-020220-1; appb.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 694 AA; 79228 MW; 2B03382D411162DC CRC64;
```

Query Match 60.1%; Score 2437; DB 13; Length 694;
Best Local Similarity 61.2%; Pred. No. 3e-141;
Matches 476; Conservative 99; Mismatches 97; Indels 106; Gaps 10;

Qy	7	LLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTK	66
Db	9	LLMLTTLTSLAIEVPSDDSVGLLAEPQVAMFCGKLNMHINVQSGKWE PDPTGTKSCISTK	68
Qy	67	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDA	126
Db	69	EGILKYCQEVYPDLQITNVVEANQPVSIQNWCKMGRQRCSRSHTHIVVPYRCLVGEFVSDA	128
Qy	127	LLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVC	186
Db	129	LLVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVC	188
Qy	187	CPLAEESDNVDSADAEEDSDVWVGADTDYADGS--EDKVV-----EVAEEEEVAEEVEE	239
Db	189	CPMEEQKD-LDSEEQEEANSVWVGGAETEYTDASVLKEQVTAKPDPAVTEDDEDLNEE	247
Qy	240	EEADDDDEDDGDEVEEEAE-----PYEEATERTTSIA--TTTTTTTESVEEVVREVCS	292
Db	248	EEVWDNDEDDGDEDEDEDEDDDEDIIDEQDTSEQTSNIAMTTTTTTTTTESIEEVVR----	303
Qy	293	EQAETGPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKT	352
Db	304	-----	303
Qy	353	TQEPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMRE	412
Db	304	-----VPTMAPSPADAVDRYLEAPGDMNEHMR FQKAKESLEAKHREKMSEVMRE	352
Qy	413	WEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLA	472
Db	353	WEEAERQAKNLPADKKTIQRFQEKVESLEKEAAGERQQLVETHMARVEALLNDRRQA	412
Qy	473	LENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMT	532
Db	413	LESYLSSLQSDQPRPRQVLNLLKKYIRAEQKDRQHTLKHFEHVREVDPKKASQIRPFVMT	472
Qy	533	HLRVIYERMNOSLSLLYNVPAVAEEIODEVDELLOKEONYSDDVLANMISEPRISYGND	592

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      ||||| ||||| || || || :|||:| |:|::| |::: |: |:| |||||
Db      473 HLRVIEERMNQSLGYLYKVPQVANDIQDQVAVLVQRDQAEVTQQLSSLQSKMRVSYGNDA 532
Qy      593 LMPSLTETKTTVELLPVNGEFSLDDLQPVHSFGADSV PANTENEVEPV DARPAADRGLTT 652
      ||| |:: |:: || : | : | || |||:| ||||| |::| |
Db      533 LMPDLPDSTTPLDNLPPEQD-GLGFIHP-ESFN----QANTDNHVEPV DARPIPERGLPT 586
Qy      653 RPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVI 712
      || || :||:| | ||:|:| |:::| |||:| ||||| |||||
Db      587 RP-----EIPKVRLDIEERHNAGYDVRDKRLMFLAEDMGSNKGAIIGLMVGGVVI 636
Qy      713 ATVIVITLVMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
      |||||:| |||||:| |||||:| |||||:| |||||:| |||||
Db      637 ATVIVITLVMLRKKQYTSIHGGVIEVDAAVTPEERHLAKMQQNGYENPTYKFFEQMQN 694

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RESULT 13

Q9I9E7

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ID      Q9I9E7          PRELIMINARY;          PRT;      612 AA.
AC      Q9I9E7;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Amyloid protein (Fragment).
GN      APPA.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Slavov D.B., Gardiner K.;
RT      "An App cDNA from Zebrafish (Danio rerio).";
RL      Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF257742; AAF71748.1; -.
DR      HSSP; P05067; 1HZ3.
DR      ZFIN; ZDB-GENE-000616-13; appa.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008155; A4_APP.
DR      InterPro; IPR008154; A4_extra.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF02177; A4_EXTRA; 1.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PRINTS; PR00203; AMYLOIDA4.
DR      PROSITE; PS00319; A4_EXTRA; 1.
DR      PROSITE; PS00320; A4_INTRA; 1.
FT      NON_TER      1      1
SQ      SEQUENCE      612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;

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Query Match          56.4%; Score 2288.5; DB 13; Length 612;
Best Local Similarity 64.7%; Pred. No. 3.3e-132;
Matches 459; Conservative 67; Mismatches 80; Indels 103; Gaps 13;

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Qy      68 GILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDAL 127
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GILQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVSDAL 60

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Qy 128 LVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCC 187
 |||:|||||:|||||:| :| |||:|||||
 Db 61 LVPDKCKFLHQERMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVCC 120

Qy 188 PLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDDED 247
 | |: || |||:|||||: || : | : : | | | :||:| |:|:
 Db 121 P-ADAGKESESAAVEEDDSVWVGAEADYTENSMTR--DAAAEPV--LEDDADEEEE 175

Qy 248 DEDGD-----EVEEEAEPEYEEATERTT-SIATTTTTTTESVEEVVREVCSEQAETGPCR 301
 |||| :||| || || |: |: :|||:||||
 Db 176 DEDGDGDRDEKIEEEEE--EERTQSTSAALTSTTTTTTESVDEVVR----- 220

Qy 302 AMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARDP 361
 Db 221 ----- 220

Qy 362 VKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQAK 421
 :|| :|| |||:|||| | |||| | ||| || |||:|||||
 Db 221 --VPTPSSSPDAVDRYLET PADENEHAHFLKAKESLET KHRERMSQVMREWEAAERQAK 278

Qy 422 NLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQ 481
 :||: |||:|||||:||||:|:|||||:|||||:|:|:
 Db 279 SLPRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRLALESYLSALQ 338

Qy 482 AVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERM 541
 | |||:|:||||| |||: ||| |||: ||| |||
 Db 339 ADPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERM 398

Qy 542 NQSLSLLYNVPAAVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGN DALMPSLTETK 601
 |||| ||| || |:|:|:| |||:| |||: | :| :|:| ||| |
 Db 399 NQSLGLLYKVPGVADDIQDQV-ELLQREQQEMSAQLANLQSDARVSYGN DALMPDST--- 454

Qy 602 TTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTNI 661
 :||| : | || || |:||||| | | ||| |||
 Db 455 AGLELLPAEDTQGF GFHP-ESFN----QPNTNQVEPVDARVPDLDLATRPVSGL--- 506

Qy 662 KTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLV 721
 | :|| |:|:| || || |:||||| |||:|||||
 Db 507 KPDDIPELRMEAEERHS---EVYHQKLVFFAEDVSSNKGAIIGLMVGGVVIATIIIVITLV 563

Qy 722 MLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 ||:|||||:|:||||| |||:|||||
 Db 564 MLRKKQYTSIHHGII EVDAAVTPEERHLSKMQQNGYENPTYKFFEQMHN 612

RESULT 14

Q61482

ID Q61482 PRELIMINARY; PRT; 763 AA.
 AC Q61482;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CDE1-binding protein CDEBP.
 GN CDEBP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6;
 RX MEDLINE=96299736; PubMed=8661100;
 RA Yang Y., Martin L., Cuzin F., Mattei M.G., Rassoulzadegan M.;
 RT "Genomic structure and chromosomal localization of the mouse CDEI-
 RT binding protein CDEBP (APLP2) gene and promoter sequences.";
 RL Genomics 35:24-29(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6;
 RA Luc M., Yang Y.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U37485; AAB38114.1; -.
 DR EMBL; U37468; AAB38114.1; JOINED.
 DR EMBL; U37469; AAB38114.1; JOINED.
 DR EMBL; U37470; AAB38114.1; JOINED.
 DR EMBL; U37471; AAB38114.1; JOINED.
 DR EMBL; U37472; AAB38114.1; JOINED.
 DR EMBL; U37473; AAB38114.1; JOINED.
 DR EMBL; U37474; AAB38114.1; JOINED.
 DR EMBL; U37475; AAB38114.1; JOINED.
 DR EMBL; U37476; AAB38114.1; JOINED.
 DR EMBL; U37477; AAB38114.1; JOINED.
 DR EMBL; U37478; AAB38114.1; JOINED.
 DR EMBL; U37479; AAB38114.1; JOINED.
 DR EMBL; U37480; AAB38114.1; JOINED.
 DR EMBL; U37481; AAB38114.1; JOINED.
 DR EMBL; U37482; AAB38114.1; JOINED.
 DR EMBL; U37483; AAB38114.1; JOINED.
 DR EMBL; U37484; AAB38114.1; JOINED.
 DR HSSP; P05067; 1MWP.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 763 AA; 86716 MW; 2CDC7780180619A6 CRC64;

Query Match 48.3%; Score 1960.5; DB 11; Length 763;
 Best Local Similarity 49.3%; Pred. No. 5.8e-112;
 Matches 400; Conservative 130; Mismatches 171; Indels 111; Gaps 21;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLLNMHMNVQNGKWDSDP 56

Db	15	LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWE PDP	74
Qy	57	SGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
Db	75	TGTKSCLGTKEEVLQYCQEIYPELQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK	132
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
Db	133	CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV	192
Qy	177	DKFRGVEFVCCPLAE--ESDNVDSADAEEDSDVWGGADTDYADGSEDKVVEVAE---E	231
Db	193	DQFHGTEYVCCPQTKTVDS DSTMSKEEEEEEE-----DEEDEEDYDLDKSEFPTE	243
Qy	232	EEVAEVEEEEEAD-DDEDDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTES	282
Db	244	ADLEDFTAAADEEEEEDEEEGEEVVEDRDYYYDPFKGDDYNE--ENPTESSEGTISDK	301
Qy	283	VEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRN NFDEEYCMVAVCG	342
Db	302	IVHDVKAVCSQEAMTGPCRAVMRWFYFDLSKGKCVRFIYGGCGGNRN NFESDYCMVAVCK	361
Qy	343	SAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLET PGDENEHAHFQKAKERLEAKH	402
Db	362	AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH	401
Qy	403	RERMSQVMREWEAEERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVE	462
Db	402	RNRMDRVKKEWEEAELQAKNLPKTERQT LIQHFQAMVKALEKEAASEKQQLVETHLARVE	461
Qy	463	AMLNDRRRRLALENYITALQAVPPRPRHVFNM LKKYVRAEQKDRQHTLKHFEHVRMVDPKK	522
Db	462	AMLNDRRRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDR LHTIRHYQHVLAVDPEK	521
Qy	523	AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMIS	582
Db	522	AAQMSQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM--	572
Qy	583	EPRISYGNDALMPSLTETKTTVELLPVNGEFS LDDLQPWHSFGADSV PANTENEVEPVDA	642
Db	573	-----DQFTSSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE----DT	614
Qy	643	RPAADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAED	694
Db	615	QPELYHPM--KKGSGMAEQDGLLIGAEKVINSKNKM DENMVIDETLDV--KEMI FNAER	670
Qy	695	VGS-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE	737
Db	671	VGGLEEEEPESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVE	730
Qy	738	VDAAVTPEERHLSKMQQNGYENPTYKFFE QMQ	769
Db	731	VDPMLTPEERHLNKMQNHYENPTYKYLEQMQ	762

Q60709

ID Q60709 PRELIMINARY; PRT; 751 AA.
AC Q60709;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid precursor-like protein 2, isoform 751.
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RA Slunt H.H., Von Koch C., Sisodia S.S.;
RT "Mouse Amyloid Precursor-Like Protein 2 (APLP2) mRNA, isoform APLP2-
RT 751, complete cds.";
RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-229 FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=94132029; PubMed=8300594;
RA Slunt H.H., Thinakaran G., Von Koch C., Lo A.C., Tanzi R.E.,
RA Sisodia S.S.;
RT "Expression of a ubiquitous, cross-reactive homologue of the mouse
RT beta-amyloid precursor protein (APP).";
RL J. Biol. Chem. 269:2637-2644(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=94350957; PubMed=8071334;
RA Thinakaran G., Sisodia S.S.;
RT "Amyloid precursor-like protein 2 (APLP2) is modified by the addition
RT of chondroitin sulfate glycosaminoglycan at a single site.";
RL J. Biol. Chem. 269:22099-22104(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RA Thinakaran G.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U15571; AAA50603.1; -.
DR PIR; A49974; A49974.
DR HSSP; P05067; 1MWP.
DR MGD; MGI:88047; Aplp2.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 85247 MW; D183F6A4AD17BC04 CRC64;

Query Match 48.2%; Score 1956.5; DB 11; Length 751;
Best Local Similarity 49.3%; Pred. No. 1e-111;
Matches 397; Conservative 130; Mismatches 169; Indels 109; Gaps 20;

Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP 56
| :||| || | : ||| :|||||||:||||:|:| |||: ||
Db 15 LLVLLLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKLNMHVNIQTGKWEPPDP 74

Qy 57 SGTKTCTIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
:||||:| ||| :|||||:|||||||:||||| | :||:| ::|||: | |||::
Db 75 TGTKSCLGTKEEVLQYCQEIYPQLQITNVMEANQPVNIDSWCRRDKRQCKS--HIVIPFK 132

Qy 117 CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI 176
||||||| ||||| |:| |||||:||| | |||: || | : |: |||||:|
Db 133 CLVGEFVSDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSYGMLLPCGV 192

Qy 177 DKFRGVFEVCCPLAE--ESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAE---E 231
|:| | |:||| : :||: | :||:: | | || :: :| |
Db 193 DQFHGTEYVCCPQTKTVDSSTMSKEEEEEEE-----DEEDEEEDYDLDKSEFPTE 243

Qy 232 EEVAEVEEEEEAD-DEDEDEDGDEVEEEAE-----EPYEEATERTTSIATTTTTTTES 282
:: : | || ::||:|:| || | : : : | | | : : | : :
Db 244 ADLEDFTEAAADEEEEDDEEGEEVVEDRDYYYDPFKGDDYNE--ENPTEPSSEGTISDK 301

Qy 283 VEEVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVAVCG 342
: | : |||::| |||||:| |||||:| || | ||||| |||||:|:| |||||
Db 302 IVHDKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNNFESDYCMVAVCK 361

Qy 343 SAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKH 402
: : | ||| : || | | |:||| |||||:| | :|
Db 362 AMI-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRH 401

Qy 403 RERMSQVMREWEAEERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVE 462
| || :| :||| ||||| ::: :||| | :||:|:|:|:|:|:|:|:|
Db 402 RNRMDRVKKEWEEAELQAKNLPKTERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVE 461

Qy 463 AMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPPK 522
|||||||:||||: |||: ||| : |:| ||| ||| |||:|:| |||:|
Db 462 AMLNDRRRIALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEK 521

Qy 523 AAQIRSQVMTHLRVIYERMNQSLSLLYNVPAVAEEIQDEVDELLQKEQNYSDDLANMIS 582
|||::| ||||| || || ||||| || |||:|:|:|:|:|:|:|:|:| :|
Db 522 AAQMKSQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM-- 572

Qy 583 EPRISYGNDAIMPSTLTETKTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDA 642
| | :|| | : | : | | | | : :|||
Db 573 -----DQFTSSISENPVDVRVSSESE-EIPPFHPLHPF-----PSLSENE----- 612

Qy 643 RPAADRGLTTRPGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS---- 697
|: : | || : : | |: || | :| :::| || ||
Db 613 ----GSGMAEQDG-GLIGAEKVINSKNKMNDENMVIDETLDV--KEMIFNAERVGGLEEE 665

Qy 698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVDAAVTP 744
: |:|||:| | |||||:||||:|:| | ||:|||| :||
Db 666 PESVGPLREDFSLSSNALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVDPM LTP 725
Qy 745 EERHLSKMQQNGYENPTYKFFEQQMQ 769
||||:||| :|||||||: ||||
Db 726 EERHLNKMQN HGYENPTYKYLEQQMQ 750

Search completed: August 13, 2004, 09:15:34
Job time : 121.521 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:28 ; Search time 28.2051 Seconds
(without alignments)
1421.515 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	4058	100.0	770	1	A4_HUMAN	P05067 h amyloid b
2	4040	99.6	770	1	A4_MACFA	P53601 m amyloid b
3	3981	98.1	770	1	A4_PIG	P79307 s amyloid b
4	3952	97.4	770	1	A4_CAVPO	Q60495 c amyloid b
5	3937	97.0	770	1	A4_RAT	P08592 r amyloid b
6	3923	96.7	770	1	A4_MOUSE	P12023 m amyloid b
7	3921.5	96.6	751	1	A4_SAIISC	Q95241 s amyloid b
8	2763.5	68.1	780	1	A4_TETFL	O73683 tetraodon f
9	2699	66.5	737	1	A4_FUGRU	O93279 fugu rubrip
10	1981.5	48.8	763	1	APP2_HUMAN	Q06481 homo sapien
11	1971.5	48.6	765	1	APP2_RAT	P15943 rattus norv
12	1704.5	42.0	695	1	APP2_MOUSE	Q06335 mus musculu
13	1159.5	28.6	650	1	APP1_HUMAN	P51693 homo sapien
14	1150.5	28.4	653	1	APP1_MOUSE	Q03157 mus musculu
15	785	19.3	686	1	A4_CAEL	Q10651 caenorhabdi
16	739	18.2	887	1	A4_DROME	P14599 drosophila
17	403	9.9	76	1	A4_MACMU	P29216 macaca mula

18	292	7.2	59	1	A4_BOVIN	Q28053	bos taurus
19	288	7.1	58	1	A4_RABIT	Q28748	oryctolagus
20	288	7.1	58	1	A4_SHEEP	Q28757	ovis aries
21	287	7.1	58	1	A4_CANFA	Q28280	canis famil
22	283	7.0	57	1	A4_URSMA	Q29149	ursus marit
23	194.5	4.8	3911	1	AKA9_HUMAN	Q99996	h a-kinase
24	186	4.6	252	1	SPT2_HUMAN	O43291	homo sapien
25	186	4.6	993	1	SCP1_MOUSE	Q62209	mus musculu
26	176	4.3	55	1	ISH1_STOHE	P31713	stoichactis
27	175	4.3	302	1	TFPI_RAT	Q02445	rattus norv
28	174.5	4.3	252	1	SPT2_MOUSE	Q9wu03	mus musculu
29	174.5	4.3	513	1	SPT1_HUMAN	O43278	homo sapien
30	173.5	4.3	1498	1	GOA3_HUMAN	Q08378	homo sapien
31	169	4.2	1875	1	MLP1_YEAST	Q02455	saccharomyc
32	168	4.1	304	1	TFPI_HUMAN	P10646	homo sapien
33	166	4.1	55	1	ISH2_STOHE	P81129	stoichactis
34	164.5	4.1	507	1	SPT1_MOUSE	Q9r097	mus musculu
35	163.5	4.0	346	1	AMBP_MERUN	Q62577	meriones un
36	163.5	4.0	1130	1	YL17_CAEEL	Q11102	caenorhabdi
37	163.5	4.0	2130	1	BA2B_CHICK	Q9de13	gallus gall
38	163	4.0	2944	1	CA17_HUMAN	Q02388	homo sapien
39	163	4.0	3176	1	CA36_HUMAN	P12111	homo sapien
40	162.5	4.0	297	1	TRT2_HUMAN	P45379	homo sapien
41	162	4.0	304	1	TFPI_MACMU	Q28864	macaca mula
42	162	4.0	407	1	IE68_HSVSA	Q01042	herpesvirus
43	162	4.0	3137	1	CA36_CHICK	P15989	gallus gall
44	161.5	4.0	630	1	YCF2_OENVI	P31569	oenothera v
45	161.5	4.0	1278	1	DYNA_HUMAN	Q14203	homo sapien

ALIGNMENTS

RESULT 1

A4_HUMAN

ID A4_HUMAN STANDARD; PRT; 770 AA.

AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;

AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease

DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease

DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-

DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42

DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);

DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)

DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-

DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)

DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)

DE (Amyloid intracellular domain 50) (AID(50)); C31].

GN APP OR A4 OR AD1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP639).

RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [14]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [15]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [16]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [17]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [18]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [19]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [20]
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
 RP AND AD GLY-717.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 RN [21]
 RP SEQUENCE OF 656-737 FROM N.A.

RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [22]

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 8.2e-196;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Qy	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Db	361	PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRRLALENYITAL	480
Qy	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661	IKTEEISEVKMDAEFRHDSGYEVVHHQKLVFFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720


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Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL 720
Qy      721 VMLKKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
Db      721 VMLKKKKQYTSIHGHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

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RESULT 2

A4_MACFA

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ID      A4_MACFA          STANDARD;          PRT;    770 AA.
AC      P53601; Q95KN7;
DT      01-OCT-1996 (Rel. 34, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE      amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE      Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE      APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE      Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE      (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE      secretase C-terminal fragment 50); C31].
GN      APP.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC      TISSUE=Cerebellum;
RX      MEDLINE=91273117; PubMed=1905108;
RA      Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT      "Homology of the amyloid beta protein precursor in monkey and human
RT      supports a primate model for beta amyloidosis in Alzheimer's
RT      disease.";
RL      Am. J. Pathol. 138:1423-1435(1991).
CC      -!- FUNCTION: Functions as a cell surface receptor and performs
CC      physiological functions on the surface of neurons relevant to
CC      neurite growth, neuronal adhesion and axonogenesis. Involved in
CC      cell mobility and transcription regulation through protein-protein
CC      interactions (By similarity). Can promote transcription activation
CC      through binding to APBB1/Tip60 and inhibit Notch signaling through
CC      interaction with Numb (By similarity). Couples to apoptosis-
CC      inducing pathways such as those mediated by G(0) and JIP (By
CC      similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC      Acts as a kinesin I membrane receptor, mediating the axonal
CC      transport of beta-secretase and presenilin 1 (By similarity). May
CC      be involved in copper homeostasis/oxidative stress through copper
CC      ion reduction. In vitro, copper-metallated APP induces neuronal
CC      death directly or is potentiated through Cu(II)-mediated low-
CC      density lipoprotein oxidation (By similarity). Can regulate
CC      neurite outgrowth through binding to components of the
CC      extracellular matrix such as heparin and collagen I and IV (By
CC      similarity). The splice isoforms that contain the BPTI domain
CC      possess protease inhibitor activity (By similarity).
CC      -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

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CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=P53601-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M58727; AAA36829.1; -.
 DR EMBL; M58726; AAA36828.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(42) (POTENTIAL).

FT	CHAIN	688	711	P3(40) (POTENTIAL).
FT	CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT	CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT	CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT	CHAIN	740	770	C31 (POTENTIAL).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	724	734	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	739	740	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 99.6%; Score 4040; DB 1; Length 770;

Best Local Similarity 99.5%; Pred. No. 6.5e-195;

Matches 766; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWSDPSGTK	60
Qy	61	TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPQLITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240

Db	181		GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE	240
Qy	241		EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Db	241		EADDDDEDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301		RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLRKTTRREPLTRD	360
Qy	361		PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361		PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421		KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421		KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481		QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541		MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	541		MNQSLSLLYNVPAAVEEIQDEVDLLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Qy	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	601		KTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Qy	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Db	661		IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL	720
Qy	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770
Db	721		VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN	770

RESULT 3

A4_PIG

ID A4_PIG STANDARD; PRT; 770 AA.
AC P79307; Q29023; Q9TUI0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(0) and JIP (By
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated

pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 CC -----

DR EMBL; AB032550; BAA84580.1; -.
 DR EMBL; Z84022; CAB06313.1; -.
 DR EMBL; X56127; CAA39592.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.

FT	SIGNAL	1	17	BY SIMILARITY.
FT	CHAIN	18	770	AMYLOID BETA A4 PROTEIN.
FT	CHAIN	18	687	SOLUBLE APP-ALPHA (POTENTIAL).
FT	CHAIN	18	671	SOLUBLE APP-BETA (POTENTIAL).
FT	CHAIN	672	770	C99 (BY SIMILARITY).
FT	CHAIN	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT	CHAIN	672	711	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT	CHAIN	688	770	C83 (BY SIMILARITY).
FT	CHAIN	688	713	P3(42) (BY SIMILARITY).
FT	CHAIN	688	711	P3(40) (BY SIMILARITY).
FT	CHAIN	712	770	GAMMA-CTF(59).
FT	CHAIN	714	770	GAMMA-CTF(57).
FT	CHAIN	721	770	GAMMA-CTF(50) (BY SIMILARITY).
FT	CHAIN	740	770	C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT	DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	700	723	POTENTIAL.
FT	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	135	155	COPPER-BINDING (BY SIMILARITY).
FT	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY
FT				SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).

FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

Query Match 98.1%; Score 3981; DB 1; Length 770;
 Best Local Similarity 97.8%; Pred. No. 5.8e-192;
 Matches 753; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGK	60
		: : : :	
Db	1	MLPGLALVLLAAWTARALEVPTDGNAGLLAEPQVAMFCGKLNMHMNVQNGKWESDPSGK	60
Qy	61	TCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Db	61	TCIGTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRSRKQCKTHTHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEEDSDVWGGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
		: : : :	
Db	181	GVEFVCCPLAEESDNIDSADAEEEDSDVWGGADTDYADGSEDKVVEVAEEEEVADVEEE	240
Qy	241	EADDDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
		:	
Db	241	EAEDDEDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTSVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVMSQSLLKTTQEHLPOD	360
Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Db	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQVLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPKADKKAVIQHFQEKVESLEQEANERQQVLVETHMARVEAMLNDRRLALENYITAL	480
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Qy	541	MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTET	600

Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLNMISEPRISYGNDALMPSLTET 600
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPV DARPAADRGLTTRPGSGLTN 660
 |||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPV DARPAADRGLTTRPGSGLTN 660
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 |||||
 Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 Qy 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||
 Db 721 VMLKKKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 4

A4_CAVPO

ID A4_CAVPO STANDARD; PRT; 770 AA.
 AC Q60495; Q60496;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing."
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta."
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor

RT protein.";

RL Neuroscience 95:243-254(2000).

RN [4]

RP GAMMA-SECRETASE PROCESSING.

RX MEDLINE=20576391; PubMed=11035007;

RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,

RA Ziani-Cherif C., Onstead L., Sambamurti K.;

RT "A novel gamma -secretase assay based on detection of the putative

RT C-terminal fragment-gamma of amyloid beta protein precursor.";

RL J. Biol. Chem. 276:481-487(2001).

CC -!- FUNCTION: Functions as a cell surface receptor and performs

CC physiological functions on the surface of neurons relevant to

CC neurite growth, neuronal adhesion and axonogenesis. Involved in

CC cell mobility and transcription regulation through protein-protein

CC interactions (By similarity). Can promote transcription activation

CC through binding to APBB1/Tip60 and inhibit Notch signaling through

CC interaction with Numb (By similarity). Couples to apoptosis-

CC inducing pathways such as those mediated by G(0) and JIP (By

CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).

CC Acts as a kinesin I membrane receptor, mediating the axonal

CC transport of beta-secretase and presenilin 1 (By similarity). May

CC be involved in copper homeostasis/oxidative stress through copper

CC ion reduction (By similarity). In vitro, copper-metallated APP

CC induces neuronal death directly or is potentiated through Cu(II)-

CC mediated low-density lipoprotein oxidation (By similarity). Can

CC regulate neurite outgrowth through binding to components of the

CC extracellular matrix such as heparin and collagen I and IV (By

CC similarity). The splice isoforms that contain the BPTI domain

CC possess protease inhibitor activity (By similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins

CC and apolipoproteins E and J in the CSF and to HDL particles in

CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.

CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the

CC extracellular matrix and may regulate neurite outgrowth in the

CC brain (By similarity).

CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved

CC peptides, including C31, are potent enhancers of neuronal

CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

CC cytoplasmic proteins, including APBB family members, the APBA

CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also

CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2

CC (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).

CC Associates with microtubules in the presence of ATP and in a

CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds

CC all three isoforms of APOE, in vitro and in vivo. When lipidated,

CC ApoE3 appears to be the preferred amyloid binding isoform, while

CC the apoE4 isoform-beta-APP40 complex is capable of being

CC transported across the blood-brain barrier.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface

CC protein that rapidly becomes internalized via clathrin-coated pits

CC (By similarity). During maturation, the immature APP (N-

CC glycosylated in the endoplasmic reticulum) moves to the Golgi

CC complex where complete maturation occurs (O-glycosylated and

CC sulfated) (By similarity). After alpha-secretase cleavage, soluble

CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similatity).

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;

CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.

CC -!- INDUCTION: Increased levels during neuronal differentiation.

CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.

CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory
 CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
 CC and amyloid-beta 42 (Abeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).

CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).

CC -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the appicans (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.

CC -!- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X97631; CAA66230.1; -.
 DR EMBL; X99198; CAA67589.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
 FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
 FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
 FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).

Query Match 97.4%; Score 3952; DB 1; Length 770;
 Best Local Similarity 96.9%; Pred. No. 1.6e-190;
 Matches 746; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSDPSGTK 60
 ||| ||||| |||||||||||||||||||||||||:|||||||: |||||
 Db 1 MLPSLALLLLTTWTARALEVPTDGNAGLLAEPQIAMFCGKLLNMHMNVQNGKWEPPDPSGTK 60
 Qy 61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
 ||| :||||||||||||||||||||||||||||| |||||||||||||||||

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Db      61 TCIGSKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRSRKQCKTHPHFVIPYRCLVG 120
Qy      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
        |||
Db      121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy      181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
        |||:|||||:|||||
Db      181 GVEFVCCPLAEESDNIDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVADVVEE 240
Qy      241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
        |||:|||||:|||||
Db      241 EADDDDEDVEDGDEVEEEAEPEYEEATEKTTSIATTTTTTTESVEEVVREVCSEQAETGPC 300
Qy      301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
        |:|||||:|||||:|::
Db      301 RSMISRWFYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSVMSQNLKTSGEFVSQG 360
Qy      361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
        |||
Db      361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
Qy      421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
        |||
Db      421 KNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Qy      481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
        |||
Db      481 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Qy      541 MNQSLSLLYNVPAAVEEQDEVDLLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTET 600
        |||
Db      541 MNQSLSLLYNVPAAVEEQDEVDLLQKEQNYSDDLANMISEPRISYGNDAIMPSTLTET 600
Qy      601 KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
        |||
Db      601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Qy      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
        |||
Db      661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
Qy      721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
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Db      721 VMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770

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RESULT 5

A4_RAT

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ID_ A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-

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DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95263526; PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=97150061; PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND

RP TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
 RT Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556(1999).
 RN [8]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024358;
 RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouilliot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Go heterotrimeric
 RT protein within a cell compartment specialized in signal
 RT transduction.";
 RL J. Neurosci. 19:1717-1727(1999).
 RN [9]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970;
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 RT splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10388-10391(1995).
 RN [10]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
 RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 RT peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616(1999).
 RN [11]
 RP BETA-AMYLOID ZINC BINDING.
 RX MEDLINE=99343552; PubMed=10413512;
 RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 RT of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX MEDLINE=21956095; PubMed=11959460;
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]

RP PHOSPHORYLATION ON SER-730.
 RX MEDLINE=99262094; PubMed=10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate E in the repeating disaccharide region
 RT and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
 CC G(0) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).

CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBL, KNS2
 CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 97.0%; Score 3937; DB 1; Length 770;
 Best Local Similarity 96.9%; Pred. No. 9.1e-190;
 Matches 746; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

```

Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDPSGTK 60

Qy     61 TCIDTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 TCIGTKEGILQYCQEVYPQLQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVG 120

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Qy    181 GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEEE 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 GVEFVCCPLAEESDSIDSADAEEDDSVWVGADTDYADGGEDKVVEVAEEEEVADVVEEEE 240

Qy    241 EADDDDEDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC 300
      ||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 EAEDDEDVEDGDEVEEEAEPEYEEATERTTSIATTTTTTTTSESVEEVVREVCSEQAETGPC 300

Qy    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSVSSQSLLKTTSEPLPQD 360

Qy    361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 PVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA 420

Qy    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQQLVETHMARVEAMLNDRRRRLALENYITAL 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQQLVETHMARVEAMLNDRRRRLALENYITAL 480

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Qy 481 QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 ||||| |||||
 Db 481 QAVPPRPHHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
 ||||| |||||
 Qy 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 ||||| |||||
 Db 541 MNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDVLANMISEPRISYGNDALMPSLTET 600
 ||||| |||||
 Qy 601 KTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 ||||| |||||
 Db 601 KTTVELLPVNGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTN 660
 ||||| |||||
 Qy 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 ||||| |||||:|
 Db 661 IKTEEISEVKMDAEFGHDSGFVVRHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITL 720
 ||||| |||||
 Qy 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
 ||||| |||||
 Db 721 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEOMQN 770
 ||||| |||||

RESULT 6

A4_MOUSE

ID A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023; P97487; P97942; Q99K32;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
 DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 DE 50) (AID(50)); C31].
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor."
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [2]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RA Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

RN [8]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of *Mus domesticus*.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-I.";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.
 RX MEDLINE=22008109; PubMed=12011466;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid

RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RT nuclear fraction of neurones in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
 CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 96.7%; Score 3923; DB 1; Length 770;
 Best Local Similarity 96.6%; Pred. No. 4.6e-189;
 Matches 744; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP

CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;

CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).

CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).

CC Extracellular zinc-binding increases binding of heparin to APP and

CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; S81024; AAD14347.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 653 751 C99 (POTENTIAL).
 FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 669 751 C83 (POTENTIAL).
 FT CHAIN 669 694 P3(42) (POTENTIAL).
 FT CHAIN 669 692 P3(40) (POTENTIAL).
 FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).
 FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).
 FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).
 FT CHAIN 721 751 C31 (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).

FT	DOMAIN	713	732	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND.
FT	SITE	652	653	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	653	654	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	668	669	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	685	685	INVOLVED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	687	687	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	692	693	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	694	695	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT				(BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL.
FT	SITE	740	743	NPXY MOTIF.

Query Match 96.6%; Score 3921.5; DB 1; Length 751;
 Best Local Similarity 96.9%; Pred. No. 5.3e-189;
 Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

Qy	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Db	1	MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSG	60
Qy	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPIRCLVG	120
Db	61	TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRDRKQCKTHPHIVIPYRCLVG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLP	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Db	181	GVEFVCCPLAEESDHVDSADAEEDDSVWVGADTDYADGSEDKVVEVAEEEEVAEVEEE	240
Qy	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Db	241	EADDDDEDGDEVEEEAEPEYEEATERTTSIATTTTTTTESVEEVVREVCSEQAETGPC	300
Qy	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPLARD	360
Db	301	RAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSV-----	344

Qy	361	PVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	420
		:	
Db	345	---IPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQA	401
Qy	421	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRRLALENYITAL	480
Db	402	KNLPKADKKAVIQHFQEKVESLEQEAAANERQQQLVETHMARVEAMLNDRRRRLALENYITAL	461
Qy	481	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	540
Db	462	QAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER	521
Qy	541	MNQSLSLLYNVPVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	600
Db	522	MNQSLSLLYNVPVAEEIQDEVDELLQKEQNYSDDLANMISEPRISYGNDALMPSLTET	581
Qy	601	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	660
Db	582	KTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN	641
Qy	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	720
Db	642	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIVITL	701
Qy	721	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	770
Db	702	VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN	751

RESULT 8

A4_TETFL

ID A4_TETFL STANDARD; PRT; 780 AA.

AC O73683;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.

OS Tetraodon fluviatilis (Puffer fish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetradontoidea; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=47145;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98252138; PubMed=9599080;

RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;

RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";

RL Gene 210:17-24(1998).

CC -!- FUNCTION: Functional neuronal receptor which couples to

CC intracellular signaling pathway through the GTP-binding protein

CC G(O) (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

Db 128 LLVPDKCKFLHQERMNQCESHLHWHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVFVC 187

Qy 187 CPLAEESDNVDSADAEEDSDVWWGGADTDYADGS-----EDKVVEVAEEEE 232
 || || :|| : : ||||| ||:| | ||| ||

Db 188 CP-AEAERDMDSTEKDADSDVWWGGADNDYSDNSMVREPEPAEQQEETRPSVVEEEEEEG 246

Qy 233 EVAEVEEEEE-----ADDEDEDGDEVEEEAEPEYEEATERTTSIA 273
 |||: :|| |||: ||:| ||:| :| |||:|

Db 247 EVAQEDDEEEEEEVLDTQDGDGEEDHEAADDEEEEDVDEIDAFGESDDVDADAPTNNVA 306

Qy 274 ---TTTTTTTESVEEVVREVCSEAETGPCRAMISRWFVDVTEGKCA-PFFYGGCGGNRN 329
 ||||| ||| :||| | : ||| :| : ||||| |

Db 307 MTTTTTTTTTESVEEVVRMFCWAHADTGPCTASMPSWYFDAVDGRMYELMYGGCGGNMN 366

Qy 330 NFDTEEYCMVCGSAMSQSLLKTTQEPLARDPVKLPPTAASPDAVDKYLETPGDENEHA 389
 ||: |||: ||| | :|| :||| ||||| |||||

Db 367 NFESEYCLSVCSV-----VPTDMPSSPDAVDHYLET PADENEHA 407

Qy 390 HFQKAKERLEAKHRERMSQVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAANE 449
 ||||| ||||| ||||| ||||| :||| ||| |||||: |||||:|

Db 408 HFQKAKESLEAKHRERMSQVMREWEAAERQAKNLPKADKKIVIQRFQEKVEALEQEAASE 467

Qy 450 RQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLKKYVRAEQKDRQHTL 509
 ||||| |||||: |||||: ||||| |||||: |||||: |||||

Db 468 RQQLVETHMARVEALLNDRRLALENYLTALQQDPPRPRHVFESLLKKYVRAEQKDRQHTL 527

Qy 510 KHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLYNVPAVAEEIQDEVDELLQKE 569
 ||||| ||||| ||: ||||| ||||| ||| ||| :|||: |||:|

Db 528 KHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKVPGVADDIQDQV-ELLQRE 586

Qy 570 QNYSDDVLANMISEPRISYGN DALMPSLTETKTTVELLPVNGEFSLDDLQPDWH--SFGAD 627
 | |||: :| :||| ||||| :||| | :| : | ||

Db 587 QAEMAQQQLANLQTDVRVSYGN DALMPDQELGDGQADLLP--QEDTLGGVG FVHPESFN-- 642

Qy 628 SVPANTENEVEPVDARPAADRGLTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQK 687
 ||||: ||||: || :||: ||| :| | :|: ||| | : |||||

Db 643 --QLNTENQVEPVD SRPTFERGVPTRP---VTGKSMEAVPELRMETEDRQSTEYEVHHQK 697

Qy 688 LVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEER 747
 ||||| ||||| ||||| |||||: |||||: |||||: |||||

Db 698 LVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLRKKQYTSIHHGIIEVDAAVTPEER 757

Qy 748 HLSKMQQNGYENPTYKFFEQMQN 770
 ||||| ||||| ||||| |||||

Db 758 HLSKMQQNGYENPTYKFFEQMQN 780

RESULT 9

A4_FUGRU

ID A4_FUGRU STANDARD; PRT; 737 AA.

AC 093279;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:

DE Beta-amyloid protein (Beta-APP) (A-beta)].

GN APP.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetradontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98252138; PubMed=9599080;
 RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";
 RL Gene 210:17-24(1998).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; AF090120; AAD13392.1; -.
 DR HSSP; P05067; 1HZ3.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 737 ALZHEIMER'S DISEASE AMYLOID A4
 FT PROTEIN HOMOLOG.
 FT CHAIN 639 681 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 19 668 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 669 689 POTENTIAL.
 FT DOMAIN 690 737 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 286 344 BPTI/KUNITZ INHIBITOR.
 FT SITE 726 729 CLATHRIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 300 301 REACTIVE BOND.

QY 719 TLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 686 TLVMLRKKQYTSIHGVEVDAAVTPEERHLARMQQNGYENPTYKFFEQMQN 737

RESULT 10

APP2_HUMAN

ID APP2_HUMAN STANDARD; PRT; 763 AA.
 AC Q06481;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
 DE (CDEI-box binding protein) (CDEBP).
 GN APLP2 OR APPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93250009; PubMed=8485127;
 RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
 RA Norris K., Foster D.C.;
 RT "Molecular cloning of the cDNA for a human amyloid precursor protein
 RT homolog: evidence for a multigene family.";
 RL Biochemistry 32:4481-4486(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=95217334; PubMed=7702756;
 RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
 RT "A human amyloid precursor-like protein is highly homologous to a
 RT mouse sequence-specific DNA-binding protein.";
 RL DNA Cell Biol. 13:1137-1143(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94035131; PubMed=8220435;
 RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
 RA Hyman B.T., Neve R.L., Tanzi R.E.;
 RT "Isolation and characterization of APLP2 encoding a homologue of the
 RT Alzheimer's associated amyloid beta protein precursor.";
 RL Nat. Genet. 5:95-99(1993).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May play a role in the regulation of hemostasis. The
 CC soluble form may have inhibitory properties towards coagulation
 CC factors. May interact with cellular G-protein signaling pathways.
 CC May bind to the DNA 5'-GTCACATG-3'(CDEI box).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q06481-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q06481-2; Sequence=VSP_000018;
 CC Name=3;
 CC IsoId=Q06481-3; Sequence=VSP_000019;
 CC -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney
 CC and endothelial tissues.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; S60099; AAC60589.1; -.
 DR EMBL; L09209; AAA35526.1; -.
 DR EMBL; Z22572; CAA80295.1; -.
 DR EMBL; L27631; AAC41701.1; -.
 DR EMBL; BC000373; AAH00373.1; -.
 DR PIR; A49321; A49321.
 DR HSSP; P05067; 1MWP.
 DR Genew; HGNC:598; APLP2.
 DR MIM; 104776; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0003677; F:DNA binding; NAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.


```

      | : |||::| |||||::| |||||::||| | ||||| |||||::|:||||| :
Db      304 HDVKAVCSQEAMTGPCRAVMPRWYFDLSKKGKCVRFIYGGCGGNRNNFESEDYCMVCKAM 363
Qy      345 MSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRE 404
      :      | ||| : || || | :||| |||||:| | :||
Db      364 I-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRN 403
Qy      405 RMSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQIVETHMARVEAM 464
      || :| :||| |||||:| :||| |::|:|:|:|:|:|:|:|:|:|
Db      404 RMDRVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAAASEKQQLVETHLARVEAM 463
Qy      465 LNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
      |||||:|||||: |||: ||| : |::||| || |::|:|:| | |::|||
Db      464 LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAA 523
Qy      525 QIRSQVMTHLRVIYERMNQSLSLLYNPAVAEEIQDEVDLLQKEQNYSDDLANMISEP 584
      |::||| || || ||||| || ||:|:|:|:|:|:|:|:|:|:|
Db      524 QMKSQVMTHLHVIEERRNQSLSLYKVPYVAQEIQEEIDELLQEQR-----ADM---- 572
Qy      585 RISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARP 644
      | |::| | |: | |::|:| | || || | :|
Db      573 -----DQFTASISETPVDVR---VSSEES-EEIPPFHPF---HPFPALPENE----DTQP 616
Qy      645 AADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVG 696
      : : |||: | || |: |:| | :| :::| || ||
Db      617 ELYHPM--KKGSGVGEQDGGGLIGAEKVINSKNKVDENMVIDETLDV--KEMIFNAERVG 672
Qy      697 S-----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVD 739
      : |:|:| | |||||:|:|:|:|:| | |::|||
Db      673 GLEEEERESVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVD 732
Qy      740 AAVTPEERHLSKMQQNGYENPTYKFFEQMQ 769
      :|||:|:| |:|:|:|:| |||
Db      733 PMLTPEERHLNKMQNHYENPTYKYLEQMQ 762

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RESULT 11

APP2_RAT

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ID APP2_RAT          STANDARD;      PRT;    765 AA.
AC P15943;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN APLP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-627 FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT difference to human and murine homologues.";

```

RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A;
 CC IsoId=P15943-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P15943-2; Sequence=VSP_000021;
 CC Name=C;
 CC IsoId=P15943-3; Sequence=VSP_000020;
 CC Name=D;
 CC IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
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 CC -----
 DR EMBL; X77934; CAA54906.1; -.
 DR EMBL; M31322; AAA42352.1; -.
 DR PIR; A35981; A35981.
 DR PIR; S42880; S42880.
 DR HSSP; P05067; 1MWP.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;
 KW Signal; Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 696 718 POTENTIAL.
 FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	218	282	ASP/GLU-RICH (HIGHLY ACIDIC).
FT	DOMAIN	308	366	BPTI/KUNITZ INHIBITOR.
FT	ACT_SITE	322	323	REACTIVE BOND (BY SIMILARITY).
FT	DISULFID	312	362	BY SIMILARITY.
FT	DISULFID	321	345	BY SIMILARITY.
FT	DISULFID	337	358	BY SIMILARITY.
FT	DOMAIN	218	229	POLY-GLU.
FT	CARBOHYD	628	628	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT	VARSPPLIC	311	365	Missing (in isoform C and isoform D).
FT				/FTId=VSP_000020.
FT	VARSPPLIC	616	627	Missing (in isoform B and isoform D).
FT				/FTId=VSP_000021.
FT	CONFLICT	575	577	DQF -> EFV (IN REF. 2).
SQ	SEQUENCE	765 AA;	86882 MW;	CF51FCCCE305A0CF CRC64;

Query Match 48.6%; Score 1971.5; DB 1; Length 765;
 Best Local Similarity 49.7%; Pred. No. 1.5e-91;
 Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

Qy	5	LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLNMHMNVQNGKWDSDP	56
		: : : : : : : : : : :	
Db	15	LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMFCGKLNMHVNIQTGWEPDP	74
Qy	57	SGTKTCIDTKEGILQYCQEVPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR	116
		: : : : : : : : : : : : : : : : : :	
Db	75	TGTKSCLGTKEEVLQYCQEIPELQITNVMEANQPVNIDSWCRRDKKQCRS--HIVIPFK	132
Qy	117	CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGI	176
		: : : : : : : : :	
Db	133	CLVGEFVSDVLLVPENCQFFHQERMEVCEKHQRWHTVVKEACLTEGMTLYSYGMLLPCGV	192
Qy	177	DKFRGVFEVCCPLAE--ESDNVDSADAEEEDSDVWWGGADTDYA-DGSEDKVVEVAEEEE	233
		: : : : : : : : : :	
Db	193	DQFHGTEYVCCPQTKVVDSDSTMSKEEEEEEEEE-----DEEEDYALDKSEFPTEADLEDFT	248
Qy	234	VAEVEEEEEADDEDEDGDEVEEEAEPEYEE-----ATERTTSIATTTTTTTESVEEVV	287
		: : : : : : : : : : : : : :	
Db	249	EAADADEDEEEEEEEEGEEVVEDRDYDYDSFKGDDYNEENPTEPSSDGTISDKIEAHDV	308
Qy	288	REVCSEQAETGPCRAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQ	347
		: : : : : : : : : : :	
Db	309	KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVCKTMI--	366
Qy	348	SLLKTTQEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMS	407
		: : :	
Db	367	-----PPTPLPT-----NDVDVYFETSADDNEHARFQKAKEQLEIRHRSRMD	408
Qy	408	QVMREWEAAERQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLND	467
		: : : : : : : : : :	
Db	409	RVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLND	468
Qy	468	RRRLALENYITALQAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIR	527
		: : : : : : : : :	
Db	469	RRRIALENYLAALQSDPPRPHRIQLALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMK	528
Qy	528	SQVMTHLRVIYERMNQSLSLLYNVPAAVEEIQDEVDELLQKEQNYSDDLANMISEPRIS	587
		: : : : : : :	

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Db      529 SQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQR-----ADM----- 574
Qy      588 YGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSV PANTENEVEPVDARPAAD 647
      |   |::|   |   |::|   |   |::|   |   |::|   |   |
Db      575 ---DQFTSSISENPVDVR---VSSEES-EEIPPFHPPF--HPFP SLSENE-----DTQP ELY 621
Qy      648 RGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-- 697
      :   : |||:   |   |   |::|   |   |   |::|   |   |::|   |   |
Db      622 HPM--KKGSGMAEQDGGGLIGAEKVINSKNKM DENMVIDETLDV--KEMIFNAERVGGLE 677
Qy      698 -----NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIH HGVVEVDAAV 742
      :   |::|::|   |   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      678 EEPDSVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLRKRQYGTISHGIVEVHPML 737
Qy      743 TPEERHLSKMQQNGYENPTYKFFEQMQ 769
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      738 TPEERHLNKMQN HGYENPTYKYLEQMQ 764

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RESULT 12

APP2_MOUSE

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ID APP2_MOUSE      STANDARD;      PRT;      695 AA.
AC Q06335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA von der Kammer H.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-246 FROM N.A.
RX MEDLINE=94032480; PubMed=8218408;
RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT "The complete cDNA coding sequence for the mouse CDEI binding
RT protein.";
RL Biochim. Biophys. Acta 1216:154-156(1993).
RN [3]
RP SEQUENCE OF 185-695 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RX MEDLINE=93129193; PubMed=1482349;
RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT "A murine sequence-specific DNA binding protein shows extensive local
RT similarities to the amyloid precursor protein.";
RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN [4]
RP SEQUENCE OF 1-35 FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=96029629; PubMed=7592716;
RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,

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RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT "The mouse APLP2 gene. Chromosomal localization and promoter
RT characterization.";
RL J. Biol. Chem. 270:25475-25480(1995).
CC -!- FUNCTION: Binds to the DNA 5'-GTCACATG-3'(CDEI box) which plays
CC an important role in the early development of embryos.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
CC (Potential).
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; Z22592; CAA80306.1; -.
DR EMBL; M97216; AAA20039.1; -.
DR EMBL; U34291; AAC52318.1; -.
DR PIR; JC1404; JC1404.
DR PIR; S38344; S38344.
DR HSSP; P05067; 1MWP.
DR MGD; MGI:88047; Aplp2.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Transmembrane; DNA-binding; Signal; Nuclear protein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 625 648 POTENTIAL.
FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 218 231 POLY-GLU.
FT DOMAIN 256 266 POLY-GLU.
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 185 189 GMLLP -> MACCC (IN REF. 3).
SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

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Qy      5  LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMFCGRLLNMHMNVQNGKWDSDP  56
      | :|||  || | :          |||      :||| ||| :||| :| ||| : ||
Db     15  LLVLLLLGLTAPAAALAGYIEALAANAGTGFAVAEPQIAMLCGKLNMHVNIQTGKWEPPD  74

Qy     57  SGTKTCIDTKEGILQYQCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR 116
      :||| :| : ||| :||| ||| :||| ||| :||| ||| | :||| : ||| : ||| :
Db     75  TGTKSCLGTKEEVLYQCQEIYPELQITNVMEANQPVNIDSWCRRDKROCKS--HIVIPFK 132

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GN APLP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98088960; PubMed=9428684;
 RA Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L., Multhaup G.,
 RA Masters C.L., Beyreuther K., Weidemann A.;
 RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
 RT expression in COS-7 cells and identification of soluble forms in the
 RT cerebrospinal fluid.";
 RL Eur. J. Biochem. 250:354-363(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98180887; PubMed=9521588;
 RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
 RA Olsen A., Tryggvason K.;
 RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
 RT 19q13.1.";
 RL Hum. Genet. 102:192-196(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=96115107; PubMed=7494461;
 RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
 RA Black I.B.;
 RT "Selective localization of amyloid precursor-like protein 1 in the
 RT cerebral cortex postsynaptic density.";
 RL Brain Res. Mol. Brain Res. 32:36-44(1995).
 RN [5]
 RP HEPARIN AND ZINC BINDING.
 RX MEDLINE=95014513; PubMed=7929392;

RA Bush A.I., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT "The amyloid beta-protein precursor and its mammalian homologues.
RT Evidence for a zinc-modulated heparin-binding superfamily.";
RL J. Biol. Chem. 269:26618-26621(1994).

RN [6]

RP INTERACTION WITH APBA2.

RX MEDLINE=99107877; PubMed=9890987;

RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,

RA Sakiyama S., Kirino Y., Suzuki T.;

RT "Interaction of a neuron-specific protein containing PDZ domains with

RT Alzheimer's amyloid precursor protein.";

RL J. Biol. Chem. 274:2243-2254(1999).

RN [7]

RP EXTRACELLULAR COPPER-BINDING.

RX MEDLINE=22130992; PubMed=12135352;

RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,

RA Reed J., Masters C.L., White A.R., Cappai R., Beyreuther K.,

RA Bayer T.A., Multhaup G.;

RT "Evidence for a copper-binding superfamily of the amyloid precursor
RT protein.";

RL Biochemistry 41:9310-9320(2000).

CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALID1, activates transcription
CC activation through APBB1 (Fe65) binding (By similarity). Couples
CC to JIP signal transduction through C-terminal binding. May
CC interact with cellular G-protein signaling pathways. Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I.

CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APBA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.

CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
CC localized to the postsynaptic density (PSD).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.

CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
CC similarity).

CC -!- PTM: N- and O-glycosylated.

CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.

CC -!- SIMILARITY: Belongs to the APP family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

DR EMBL; U48437; AAB96331.1; -.
DR EMBL; AD000864; AAB50173.1; -.
DR EMBL; BC012889; AAH12889.1; -.
DR HSSP; P05067; 1MWP.
DR Genew; HGNC:597; APLP1.
DR MIM; 104775; -.
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.

FT	SIGNAL	1	38	POTENTIAL.
FT	CHAIN	39	650	AMYLOID-LIKE PROTEIN 1.
FT	CHAIN	621	650	C30 (BY SIMILARITY).
FT	DOMAIN	39	580	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	581	603	POTENTIAL.
FT	DOMAIN	604	650	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	158	178	COPPER-BINDING (BY SIMILARITY).
FT	DOMAIN	204	211	ZINC-BINDING.
FT	DOMAIN	310	342	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	410	441	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	442	459	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	640	643	CLATHRIN-BINDING (POTENTIAL).
FT	DOMAIN	241	247	POLY-GLU.
FT	DOMAIN	264	268	POLY-GLU.
FT	SITE	167	167	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT	SITE	604	615	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	620	621	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	638	641	ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT	SITE	640	643	NPXY MOTIF.
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	461	461	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	551	551	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	48	48	A -> P (IN REF. 1).
SQ	SEQUENCE	650 AA;	72176 MW;	B95F0F4D1C5CBAC7 CRC64;

Query Match 28.6%; Score 1159.5; DB 1; Length 650;
Best Local Similarity 35.7%; Pred. No. 4.8e-51;
Matches 276; Conservative 114; Mismatches 229; Indels 155; Gaps 17;

Qy 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
: || | || | : | : | | : | || | : | :: : | : | || ::
Db 23 LLPLLLLLLRAQPAIGSLAGGSPGAAEAPGSAQVAGLCGRLLTLHRDLRTGRWEPDPQRSR 82

DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
 GN APLP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93066322; PubMed=1279693;
 RA Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
 RA Solomon F.;
 RT "Identification of a mouse brain cDNA that encodes a protein related
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP COLLAGEN-BINDING.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RP INTERACTION WITH DAB1.
 RX MEDLINE=99389880; PubMed=10460257;
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1.";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RP INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,

RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
 RP TYR-641.
 RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamio L.;
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RT secretase regulates transcription.";
 RL J. Biol. Chem. 277:44195-44201(2002).

CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, ALID1, activates transcription
 CC activation through APBB1 (Fe65) binding. Couples to JIP signal
 CC transduction through C-terminal binding. May interact with
 CC cellular G-protein signaling pathways. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB and APBA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N- and O-glycosylated.
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: Belongs to the APP family.

CC -----
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 CC -----

DR EMBL; L04538; AAA37247.1; -.
 DR EMBL; BC021877; AAH21877.1; -.
 DR PIR; A46362; A46362.
 DR HSSP; P05067; 1MWP.
 DR MGD; MGI:88046; Aplp1.
 DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.

FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	653	AMYLOID-LIKE PROTEIN 1.
FT	CHAIN	624	653	C30 (BY SIMILARITY).
FT	DOMAIN	38	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	606	POTENTIAL.
FT	DOMAIN	607	653	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	157	177	COPPER-BINDING.
FT	DOMAIN	203	210	ZINC-BINDING (BY SIMILARITY).
FT	DOMAIN	313	345	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	413	444	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	445	462	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	263	271	POLY-GLU.
FT	DOMAIN	535	538	POLY-SER.
FT	DOMAIN	601	606	POLY-LEU.
FT	SITE	166	166	REQUIRED FOR COPPER(II) REDUCTION (BY
FT				SIMILARITY).
FT	SITE	607	618	BASOLATERAL SORTING SIGNAL (BY
FT				SIMILARITY).
FT	SITE	623	624	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	641	644	ENDOCYTOSIS SIGNAL.
FT	SITE	643	646	NPXY MOTIF.
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	554	554	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MUTAGEN	641	641	Y->G: REDUCED BINDING OF APBB1.
FT	CONFLICT	17	17	P -> PP (IN REF. 2).
SQ	SEQUENCE	653 AA;	72750 MW;	56516DC3EA40E4B0 CRC64;

Query Match 28.4%; Score 1150.5; DB 1; Length 653;
 Best Local Similarity 35.4%; Pred. No. 1.4e-50;
 Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

Qy	1	MLPGLALLLLAAWTARA-LEVPTDGNAGLLAEPQIAMFCGRILNMHMNVQNGKWSDPSGT	59
		: : : : : :: : : :	
Db	22	LLP-LSLLLLRAQLAVGNLAVGSPSAEAPGSAQVAGLCGRILTLLRDLRTGRWEPPQRS	80
Qy	60	KTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHF-VIPYRCL	118
		: : : : : : : : : : : : :	
Db	81	RRCLLDPQRVLEYCRQMPYELHIAVEQAAQAI PMERWCGGTRSGRCAHPHHEVVVPHCL	140
Qy	119	VGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDK	178
		: : : : : : :	
Db	141	PGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQAEACSSQGLILHGSGMILLPCGSDR	200
Qy	179	FRGVEFVCCPLAEESDNVDSADAEEDSDVW-WGGADTDYADGSEDKVVEVAEEEEVAEV	237
		: : : : :	
Db	201	FRGVEYVCCP-PPATPNPSGMAAGDPSTRSWPLGGR----AEGGED-----EEEVESF	248
Qy	238	EEEEADDDDEDDGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQAET	297


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      : | : : | | | | : |
Db      249 PQPVDYFVEPPQAEAAAAAAAAEERAPPPSSHTP----- 281
Qy      298 GPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMSQSLLKTTQEPL 357
      | : | | |
Db      282 ----VMVSR-----VT----- 288
Qy      358 ARDPVKLPPTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAE 417
      | | | | | | | | : | | : | | : : : | | | | | :
Db      289 ---PTPRPT-----DGVDVYFGMPGEIGEHEGFLRAKMDLEERRMRQINEVMREWAMAD 339
Qy      418 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQVLVETHMARVEAMLNDRRLALENYI 477
      | : | | | | | : : | | : : | | : : | | | | | | : :
Db      340 SQSKNLPKADRQALNEHFQSILQTLQVSGERQRLVETHATRVIALINDQRRAALEGFL 399
Qy      478 TALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVI 537
      | | | | | : | | : : | | | : : | | : : | | | | : |
Db      400 AALQGDPPQAERVLMAALRRYLRAEQKEQRHTLRHYQHVAAVDPEKAQQMRQVQVTHLQVI 459
Qy      538 YERMNQSLSLLYNVPAVAEEIQDEVDLLQKEQNYSDVLANMISEPRISYGNDAIMP-S 596
      | | | | | | | | | : | : : : : | | | | : : | | |
Db      460 EERMNQSGLLDQNPHLAQELRPQIQELL-----LAEHLGPSEL----DASVPGS 505
Qy      597 LTETKTTVELLPVNGEFSLDDLQPWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGS 656
      : | | | | | | | | | : : | | | : | | : |
Db      506 SSEDK-----GSLQP-----PESKDDPPVTLTP---KGSTDQESS 536
Qy      657 GLTNIKTEEISEVKMDAEFRHDSGYEVHH---QKLVFFAEDVGSNKGAIIGLMVGGVVIA 713
      | : : : : | : | : | : : | : : | : : |
Db      537 SSGREKLTPLEQYEQKVNASAPRGFPFHSDDIQDELAPSGTGVSRREALSGLLIMGAGGG 596
Qy      714 TVIVITLVML-KKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQ 767
      : : | : : | | | | : | | | | | : | | : : | : | : | : | : |
Db      597 SLIVLSLLLLRKKKPYGTISHGVVEVDPMLTLEEQQRLRELQRHGYENPTYRFL 651

```

RESULT 15

A4_CAEEL

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ID      A4_CAEEL          STANDARD;          PRT;      686 AA.
AC      Q10651; Q18583; Q95ZX1;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Beta-amyloid-like protein precursor.
GN      APL-1 OR C42D8.8.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE OF 6-686 FROM N.A.
RC      STRAIN=Bristol N2;
RX      MEDLINE=94089766; PubMed=8265668;
RA      Daigle I., Li C.;
RT      "apl-1, a Caenorhabditis elegans gene encoding a protein related to
RT      the human beta-amyloid protein precursor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:12045-12049(1993).

```

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Hallsworth K.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=a;
 CC IsoId=Q10651-1; Sequence=Displayed;
 CC Name=b;
 CC IsoId=Q10651-2; Sequence=VSP_000017;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the APP family.
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 CC -----
 DR EMBL; U00240; AAC46470.1; ALT_INIT.
 DR EMBL; U56966; AAA98722.1; -.
 DR EMBL; U56966; AAK68242.1; -.
 DR PIR; T15795; T15795.
 DR HSSP; P05067; 1MWP.
 DR WormPep; C42D8.8a; CE04209.
 DR WormPep; C42D8.8b; CE27845.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 KW Signal; Transmembrane; Amyloid; Neurogenesis; Glycoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 686 BETA-AMYLOID-LIKE PROTEIN.
 FT DOMAIN 22 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 686 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 205 228 ASP-RICH.
 FT DOMAIN 676 679 CLATHRIN-BINDING (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 538 539 Missing (in isoform b).
 FT /FTId=VSP_000017.
 SQ SEQUENCE 686 AA; 79434 MW; A0816858FDD48608 CRC64;

Query Match 19.3%; Score 785; DB 1; Length 686;
Best Local Similarity 26.8%; Pred. No. 2.7e-32;
Matches 224; Conservative 111; Mismatches 272; Indels 230; Gaps 23;

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Qy      1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
      :: || : : | | | | | | | | : | || | : | : | | : |
Db      6 LMIGLLIPILVA-TVYAEGSPAGSKRHEKFIPMVAFSCGYRNQYM-TEEGSWKTDDERYA 63

Qy     61 TCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG 120
      || | | : | : | : | | : | : | : | : | | | | : |
Db     64 TCFSGKLDILKYCRKAYPSMNITNIVEYSHEVSISDWCREEGSPCK-WTHSVRPYHCIDG 122

Qy    121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN-----LHDYGMLLPC 174
      || | : || || | : | | | | : || | : | | : : : : | ||
Db    123 EFHSEALQVPHDCQFQSHVNSRDQCNDYQHWKDEAGKQCKTKKSKGNKDMIVRSFAVLEPC 182

Qy    175 GIDKFRGVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEVAEEEEEV 234
      : | | | | | | | | : | : | : | : |
Db    183 ALDMFTGVFVCCP----NDQTNKTDVQKTK----- 209

Qy    235 AEVEEEEEADDEDEDEDEGDEVEEEAEPEYEEATERTTSIATTTTTTTTESVEEVVREVCSEQ 294
      | : | : | | | | | | : | | : : | | |
Db    210 ---EDEDDDDDEDDAYEDDYSEESDEKDEE----- 236

Qy    295 AETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMAVCGSAMSQSLLKTTQ 354
Db    237 ----- 236

Qy    355 EPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWE 414
      || : : || | : | | | | : | : | | : | : | : | : |
Db    237 EPSSQDP-----YFKIANWTNEHDDFKKAEMRMDEKHKRKKVDKVMKEWG 280

Qy    415 EA-----ERQAKNLPKADKKAVIQ---HFQEKVESLEQEAANERQQVLVETHMARVEAMLN 466
      : | : | : | : | : | | | : | | | : | : : | | | : |
Db    281 DLETRYNEQKAKD-PKGAEKFKSQMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLN 339

Qy    467 DRRRLALENYITAL--QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
      : : : | | : | | | | | | | | | : | : | | : | : |
Db    340 EKKRDATHDYRQALATHVKNPNKHSVLQSLKAYIRAEKDRMHTLNRYRHLLKADSKEAA 399

Qy    525 QIRSQVMTHLRVIYERMNQSLSLLYNVP-----AVA--EEIQDEVDELLQKEQNYS 573
      : | : | | | : | : | : | : | | | : : : | | : |
Db    400 AYKPTVIHRLRYIDLRLINGTLAMLRDFPDLEKYVRPIAVTYWKDYRDEVSPDISVE---- 455

Qy    574 DDVLANMISEPRISYGN--DALMPSLT----ETKTTVELLPVNGEFSLDDLQPWHSFGAD 627
      | | : | : | | | : | : | : | : | : | : | : |
Db    456 DSELTPIIHDEFKSKNAKLDVKAPTITAKPVKETDNAKVLPTASDSEEEADEYYEDED 515

Qy    628 SVPANT---ENEVEPVDPARP-----AADRGLTTRPGSGLTNIKT 663
      | : : | : | : | | | | | | | | | | | : :
Db    516 EQVKKTPDMKKKVVDIKPKEIKVTIEEEKKAPKLVETSVQTDDEDDDEDSSSSTSES 575

Qy    664 EE-----ISEVKMDAE-----FRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG 709
      : | | : : | | : | | | : | | | : :
Db    576 DEDEDKNIKELRVDIEPIIDEPASFYRHD-----KLIQSPEVERSASSVFQPYVLAS 627

Qy    710 VVIATVIVITLVMLKKKQYTSIHGCVVEVDAAVTPEERHLSKMQQNGYENPTYKFFE 766
```

Db : | | | : | : | | | | | | | | : : | | | | | | | | | :
628 AMFITAICIIAFAITNARRRRRAMRGFIEVD-VYTPEERHVAGMQVNGYENPTYSFED 683

Search completed: August 13, 2004, 09:13:17
Job time : 32.2051 secs